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(54) Title: **NOVEL G PROTEIN-COUPLED RECEPTORS**

(57) Abstract: The present invention provides a gene encoding a G protein-coupled receptor termed nGPCR-x; constructs and recombinant host cells incorporating the genes; the nGPCR-x polypeptides encoded by the gene; antibodies to the nGPCR-x polypeptides; and methods of making and using all of the foregoing.

SEQ ID NO:79, SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89,  
SEQ ID NO:93 and SEQ ID NO:185.

8. The isolated nucleic acid molecule of claim 1 wherein said nucleic acid  
5 molecule is DNA.
9. The isolated nucleic acid molecule of claim 1 wherein said nucleic acid  
molecule is RNA.
10. 10. An expression vector comprising a nucleic acid molecule of any one of claims  
1 to 5.
11. The expression vector of claim 10 wherein said nucleic acid molecule  
comprises a sequence selected from the group of odd numbered sequences consisting  
15 of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:185.
12. The expression vector of claim 10 wherein said nucleic acid molecule  
comprises a nucleotide sequence selected from the group consisting of: SEQ ID  
NO:1, SEQ ID NO:73, SEQ ID NO:9, SEQ ID NO:77, SEQ ID NO:11, SEQ ID  
20 NO:79, SEQ ID NO: 21, SEQ ID NO:81 SEQ ID NO:53, SEQ ID NO:83, SEQ ID  
NO:59, SEQ ID NO:85, SEQ ID NO:63, SEQ ID NO:87, SEQ ID NO:89, SEQ ID  
NO:67, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO: 3, and SEQ ID NO: 185.
13. The expression vector of claim 10 wherein said nucleotide sequence is  
25 selected from the group consisting of: SEQ ID NO: 73, SEQ ID NO:77, SEQ ID  
NO:79, SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89, SEQ ID  
NO:93 and SEQ ID NO: 185.
14. The expression vector of claim 10 wherein said vector is a plasmid.
- 30 15. The expression vector of claim 10 wherein said vector is a viral particle.
16. The expression vector of claim 15 wherein said vector is selected from the  
group consisting of adenoviruses, baculoviruses, parvoviruses, herpesviruses,

SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO: 86;  
SEQ ID NO:90; and SEQ ID NO:94.

- 5
60. The method of claim 57 wherein said activity is neuropeptide binding.
61. The method of claim 57 wherein said activity is neuropeptide signaling.
62. A compound identified by the method of claim 57.
- 10 63. A method of identifying an animal homolog of nGPCR-x comprising the steps:
- a) comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being
- 15 at least 10 nucleotides; and
- b) identifying nucleic acid sequences of the animal that are homologous to said sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof.
- 20
64. The method of claim 63 wherein comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being at least 10 nucleotides is performed by DNA hybridization.
- 25
65. The method of claim 63 wherein comparing the nucleic acid sequences of the animal with a sequence selected from the group of odd numbered sequence consisting of SEQ ID NO: 1 to SEQ ID NO: 93, SEQ ID NO: 185, and portions thereof, said portions being at least 10 nucleotides is performed by computer homology search.
- 30
66. A method of screening a human subject to diagnose a disorder affecting the brain or genetic predisposition therefor, comprising the steps of:
- (a) assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering an amino acid sequence, expression, or biological

(c) performing a polynucleotide migration assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences; and

(d) performing a restriction endonuclease digestion to determine  
5 whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences.

71. A method according to claim 70 wherein the assaying step comprises:  
performing a polymerase chain reaction assay to amplify nucleic acid comprising  
10 nGPCR-40 or nGPCR-54 coding sequence, and determining nucleotide sequence of the amplified nucleic acid.

72. A method of screening for an nGPCR-40 or nGPCR-54 hereditary schizophrenia genotype in a human patient, comprising the steps of:

15 (a) providing a biological sample comprising nucleic acid from said patient, said nucleic acid including sequences corresponding to alleles of nGPCR-40 or nGPCR-54; and

(b) detecting the presence of one or more mutations in the nGPCR-40 allele or the nGPCR-54 allele;

20 wherein the presence of a mutation in an nGPCR-40 allele or nGPCR-54 allele is indicative of a hereditary schizophrenia genotype.

73. The method according to claim 72 wherein said biological sample is a cell sample.

25

74. The method according to claim 72 wherein said detecting the presence of a mutation comprises sequencing at least a portion of said nucleic acid, said portion comprising at least one codon of said nGPCR-40 or nGPCR-54 alleles.

30 75. The method according to claim 72 wherein said nucleic acid is DNA.

76. The method according to claim 72 wherein said nucleic acid is RNA.

28. The nucleic acid molecule of claim 27 wherein said molecule is an antisense oligonucleotide directed to a region of a sequence selected from the group of odd numbered sequences consisting of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:  
5 185.

29. The nucleic acid molecule of claim 28 wherein said oligonucleotide is directed to a regulatory region of a sequence selected from the group of odd numbered sequences consisting of SEQ ID NO:1 to SEQ ID NO:93 and SEQ ID NO:185.

10

30. The nucleic acid molecule of claim 27 wherein said molecule is an antisense oligonucleotide directed to a region of nucleotide sequence selected from the group consisting of: SEQ ID NO: 73, SEQ ID NO:77, SEQ ID NO:79; SEQ ID NO:81 SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:89, SEQ ID NO:93 and SEQ ID NO: 185.

15

31. A composition comprising a nucleic acid molecule of any one of claims 1 to 5 or 27 and an acceptable carrier or diluent.

32. A composition comprising a recombinant expression vector of claim 10 and an  
20 acceptable carrier or diluent.

33. A method of producing a polypeptide that comprises a sequence selected from the group of even numbered sequences consisting SEQ ID NO: 2 to SEQ ID NO: 94 and SEQ ID NO: 186, and homologs and fragments thereof, said method comprising  
25 the steps of:

- a) introducing a recombinant expression vector of claim 10 into a compatible host cell;
- b) growing said host cell under conditions for expression of said polypeptide; and
- 30 c) recovering said polypeptide.

34. The method of claim 33 wherein said host cell is lysed and said polypeptide is recovered from the lysate of said host cell.

43. A composition comprising a polypeptide of claim 36 and an acceptable carrier or diluent.
- 5 44. An isolated antibody which binds to an epitope on a polypeptide of claim 36.
45. The antibody of claim 44 wherein said antibody is a monoclonal antibody.
46. A composition comprising an antibody of claim 44 and an acceptable carrier  
10 or diluent.
47. A method of inducing an immune response in a mammal against a polypeptide of claim 36 comprising administering to said mammal an amount of said polypeptide sufficient to induce said immune response.
- 15 48. A method for identifying a compound which binds nGPCR-x comprising the steps of:
- a) contacting nGPCR-x with a compound; and
  - b) determining whether said compound binds nGPCR-x.
- 20 49. The method of claim 48 wherein the nGPCR-x comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 74; SEQ ID NO: 4, SEQ ID NO: 186; SEQ ID NO: 10, SEQ ID NO: 78; SEQ ID NO: 12, SEQ ID NO: 80; SEQ ID NO: 22, SEQ ID NO: 82; SEQ ID NO: 54, SEQ ID NO: 84; SEQ  
25 ID NO: 60, SEQ ID NO: 86; SEQ ID NO: 64, SEQ ID NO: 88, SEQ ID NO: 90; SEQ ID NO: 68, SEQ ID NO: 92, and SEQ ID NO: 94.
50. The method of claim 48 wherein the nGPCR-x comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 74; SEQ ID NO: 186;  
30 SEQ ID NO: 78; SEQ ID NO: 80; SEQ ID NO: 82; SEQ ID NO: 84; SEQ ID NO: 86; SEQ ID NO: 90; and SEQ ID NO: 94.
51. The method of claim 48 wherein binding of said compound to nGPCR-x is determined by a protein binding assay.

80. A purified and isolated polynucleotide comprising a nucleotide sequence encoding an nGPCR-40 or nGPCR-54 allelic variant identified according to claim 79.

81. A host cell transformed or transfected with a polynucleotide according to  
5 claim 80 or with a vector comprising the polynucleotide.

82. A purified polynucleotide comprising a nucleotide sequence encoding nGPCR-40 or nGPCR-54 of a human with schizophrenia;

wherein said polynucleotide hybridizes to the complement of SEQ ID  
10 NO:83 or of SEQ ID NO:85 under the following hybridization conditions:

(a) hybridization for 16 hours at 42°C in a hybridization solution comprising 50% formamide, 1% SDS, 1 M NaCl, 10% dextran sulfate and

(b) washing 2 times for 30 minutes at 60°C in a wash solution comprising 0.1x SSC and 1% SDS; and

15 wherein the polynucleotide that encodes nGPCR-40 or nGPCR-54 amino acid sequence of the human differs from SEQ ID NO:84 or SEQ ID NO:86 by at least one residue.

83. A vector comprising a polynucleotide according to claim 82.  
20

84. A host cell that has been transformed or transfected with a polynucleotide according to claim 82 and that expresses the nGPCR-40 or nGPCR-54 protein encoded by the polynucleotide.

25 85. A host cell according to claim 84 that has been co-transfected with a polynucleotide encoding the nGPCR-40 or nGPCR-54 amino acid sequence set forth in SEQ ID NO:84 or SEQ ID NO:86 and that expresses the nGPCR-40 or nGPCR-54 protein having the amino acid sequence set forth in SEQ ID NO:84 or SEQ ID NO:86.

30 86. A method for identifying a modulator of biological activity of nGPCR-40 or nGPCR-54 comprising the steps of:

a) contacting a cell according to claim 84 in the presence and in the absence of a putative modulator compound;

90. An method according to claim 89 wherein the composition comprises a cell transformed or transfected with a polynucleotide that encodes nGPCR-40 or nGPCR-54.

5 91. A method of purifying a G protein from a sample containing said G protein comprising the steps of:

a) contacting said sample with a polypeptide of claim 1 for a time sufficient to allow said G protein to form a complex with said polypeptide;

b) isolating said complex from remaining components of said  
10 sample;

c) maintaining said complex under conditions which result in dissociation of said G protein from said polypeptide; and

d) isolating said G protein from said polypeptide.

15 92. The method of claim 91 wherein said sample comprises an amino acid sequence selected from the group of even numbered sequences consisting of SEQ ID NO:2 to SEQ ID NO:94 and SEQ ID NO:186.

93. The method of claim 91 wherein said polypeptide comprises an amino acid  
20 sequence homologous to a sequence selected from the group of even numbered sequences consisting of SEQ ID NO:2 to SEQ ID NO:94 and SEQ ID NO:186.

94. The method of claim 91 wherein said polypeptide comprises an amino acid  
sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 74; SEQ  
25 ID NO: 4, SEQ ID NO: 186; SEQ ID NO:10, SEQ ID NO:78; SEQ ID NO:12, SEQ  
ID NO:80; SEQ ID NO: 22, SEQ ID NO:82; SEQ ID NO:54, SEQ ID NO:84; SEQ  
ID NO:60, SEQ ID NO: 86; SEQ ID NO:64, SEQ ID NO: 88, SEQ ID NO:90; SEQ  
ID NO:68, SEQ ID NO: 92, and SEQ ID NO:94.

30 95. The method of claim 91 wherein said polypeptide comprises an amino acid  
sequence selected from the group consisting of: SEQ ID NO: 74; SEQ ID NO: 186;  
SEQ ID NO:78; SEQ ID NO:80; SEQ ID NO:82; SEQ ID NO:84; SEQ ID NO: 86;  
SEQ ID NO:90; and SEQ ID NO:94.



## SEQUENCE LISTING

<110> Pharmacia & Upjohn Company  
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<120> Novel G Protein Coupled Receptors

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gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac 360  
cgacggggat ctggggcccca tgcgccggca cagcacccac agagagaaga ggttgcccgg 420  
gatgctgacc gccgccacca gcgagtacac cacgggcagg gccaccgcga tcgccgggtt 480  
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<210> 8  
<211> 169  
<212> PRT  
<213> H.Sapiens

<400> 8

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1 5 10 15  
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20 25 30  
Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro  
35 40 45  
Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala  
50 55 60  
Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp  
65 70 75 80  
Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala  
85 90 95

Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg  
 100 105 110  
 Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg  
 115 120 125  
 Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr  
 130 135 140  
 Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala  
 145 150 155 160  
 Leu Gly Ile Ile Thr Cys Phe Asp Val  
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 <211> 270  
 <212> DNA  
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 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct cctgggcatac 180  
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<210> 10  
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 1 5 10 15  
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 20 25 30  
 Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val  
 35 40 45  
 Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg  
 50 55 60  
 Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly  
 65 70 75 80  
 Arg Thr Leu Ala Met Ala Ala Ala Ala Trp  
 85 90

<210> 11  
 <211> 888

<212> DNA  
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 gatttccctc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 180  
 tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc 240  
 gggagcatcg tgttccttac ggtggtggct gcggacaggt atttcaaagt ggtccacccc 300  
 caccacgcgg tgaacactat ctccacccgg gtggcggctg gcatcgtctg caccctgtgg 360  
 gccctgggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 420  
 acggcgcgtc cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg 480  
 ttccagctgg agttctttat gccctcggc atcatcttat ttgctcctt caagattggt 540  
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 ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg 720  
 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 780  
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 <211> 296  
 <212> PRT  
 <213> H.Sapiens

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 Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu  
 35 40 45  
 Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly  
 50 55 60  
 Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala  
 65 70 75 80  
 Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys  
 85 90 95



Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala  
 100 105 110  
 Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val  
 115 120 125  
 Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser  
 130 135 140  
 Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met  
 145 150 155 160  
 Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser  
 165 170 175  
 Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln  
 180 185 190  
 Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val  
 195 200 205  
 Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu  
 210 215 220  
 Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu  
 225 230 235 240  
 His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu  
 245 250 255  
 Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu  
 260 265 270  
 Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln  
 275 280 285  
 Arg Pro Glu Glu Met Pro Ile Ser  
 290 295

<210> 13  
 <211> 510  
 <212> DNA  
 <213> H.Sapiens

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 tgcaagctgg tgcacttctt gttctatata aacctttacg gcagcatcct gctgctgacc 180  
 tgcatctctg tgcaccagtt cctaggtgtg tgccacccac tgtgttcgct gccctaccgg 240  
 acccgagggc atgcctggct gggcaccagc accacctggg ccctgggtgg cctccagctg 300  
 ctgcccacac tggccttctc ccacacggac tacatcaatg gccagatgat ctggtatgac 360  
 atgaccagcc aagagaattt tgatcggtt tttgcctacg gcatagttct gacattgtct 420

ggcttttcttt ccctccttgg tcatttttgggt gtgctattca ctgatgggtca ggagcctgat 480  
 caagccagag gagaacctca tgaggacagg 510

<210> 14  
 <211> 170  
 <212> PRT  
 <213> H.Sapiens

<400> 14

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 Leu Tyr Val Leu Leu Pro Phe Leu Ile Ile Thr Tyr Ser Leu Asp Asp  
 20 25 30  
 Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe  
 35 40 45  
 Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val  
 50 55 60  
 His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg  
 65 70 75 80  
 Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val  
 85 90 95  
 Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile  
 100 105 110  
 Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp  
 115 120 125  
 Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser  
 130 135 140  
 Leu Leu Gly His Phe Gly Val Leu Phe Thr Asp Gly Gln Glu Pro Asp  
 145 150 155 160  
 Gln Ala Arg Gly Glu Pro His Glu Asp Arg  
 165 170

<210> 15  
 <211> 894  
 <212> DNA  
 <213> H.Sapiens

<220>  
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 <222> (431)..(461)  
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ggctccacct gggctcgccg accaggccgc tgcacccgct ggggccttca gccggtgccg 240
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cagagacgtt nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nagtactagc gcaccacaaa 480
ccccgacccc cgcgccagca gcagtgccag cagccagccc agggcggcga gggcacgcgc 540
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cagagagtgg gccgagggcg cccgcccgga tgccctgcagc agctgcagga agcggcacgc 660
caggtcccc gtggccgcgc ggggctcgcc cagcagttcc caggccagct gtgacagcgc 720
cgtgcccccg cagcggtaca ggtccgccag ggccagctgc accagcagga agtccattt 780
gcgacgcttn nnnnnnnnnn nnnnnnnnnn nnnnnnnnac aggcggcaca gcactgtggt 840
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<210> 16
<211> 296
<212> PRT
<213> H.Sapiens

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<220>
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<223> Xaa is Unknown

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<400> 16

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Arg Val Arg Leu Val Phe Leu Gly Val Ile Leu Val Val Ala Val Ala
1           5           10           15

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Gly Asn Thr Thr Val Leu Cys Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20           25           30

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Xaa Xaa Xaa Lys Arg Arg Lys Met Asp Phe Leu Leu Val Gln Leu Ala
35           40           45

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Leu Ala Asp Leu Tyr Ala Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala

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50	55	60
Trp Glu Leu Leu Gly Glu Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys 65 70 75 80		
Arg Phe Leu Gln Leu Leu Gln Ala Ser Gly Arg Gly Ala Ser Ala His 85 90 95		
Leu Val Val Leu Ile Ala Leu Glu Arg Arg Arg Ala Val Arg Leu Pro 100 105 110		
His Gly Arg Pro Leu Pro Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu 115 120 125		
Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe Val Val Arg Tyr Xaa 130 135 140		
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Leu Gln Pro Gly 145 150 155 160		
Ala Pro Leu Ser Ala Arg Ala Trp Pro Gly Met Arg Arg Cys His Trp 165 170 175		
Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr 180 185 190		
Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala 195 200 205		
Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro 210 215 220		
Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro 225 230 235 240		
Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu 245 250 255		
Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu 260 265 270		
Glu Ala Ala Trp Ser Ser Gly Pro Ala Gly Glu Trp Glu Gly Glu Ala 275 280 285		
Leu Ser Ala Cys Cys Ala Trp Trp 290 295		

<210> 17  
 <211> 801  
 <212> DNA  
 <213> H.Sapiens

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ggggaggagg tagaatagga aggaggtgac ctggatgatg aaattgtaga tccacatggg	180

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cttgatgacc gtacaggtgg ccgaacctgg gaccagggac ccattgggga agtagtgga 240
cttgatgcca tggatgctgg tggtgggcag ggagaagagc acggagaagc cccagacgat 300
gccgaggatc ctgagggccc ggcgccgggt gctctgcagt ttggcgcgga acgggtgtag 360
gatggccacg tagcgctcca cgctgacggt ggtgatgctg aggatggagg cgaagcacac 420
ggtctcaaag agggccgtct tgaagtagca gcccacgggc ccgaacaaga :agggtagtt 480
gcgccacatc tcatagacct ccaggggcat tccaaggagc aggaccagga ggtcagagac 540
cgccaggctg aagaggtagt agttggtggg cgtcttcata gcctggtgct gcagaatcac 600
caggcacacc aggacattgc caatgacccc caccacaaaa attggcacat acaccacaga 660
cacggggagg aagaagtggc tgcgccgagg tccgcagagg aaggccagat actcctcggt 720
gctgttcagg tgtttctgga atggatcttc tagtttctgc tggtagatcc aggaagcatt 780
ctgaagtttt tccatccctg a 801

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<210> 18  
 <211> 249  
 <212> PRT  
 <213> H.Sapiens

<400> 18

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1          5          10          15
Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
20        25        30
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
35        40        45
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
50        55        60
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Asn Thr
65        70        75        80
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
85        90        95
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
100       105       110
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
115       120       125
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
130       135       140
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
145       150       155       160

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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe  
 165 170 175  
 Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro  
 180 185 190  
 Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro  
 195 200 205  
 Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr  
 210 215 220  
 Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu  
 225 230 235 240  
 Arg Val Ser Ile Ala Gly Val Ala Gly  
 245

<210> 19  
 <211> 222  
 <212> DNA  
 <213> H.Sapiens

<400> 19  
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 attgtctatg catttatgaa tgaaaacttc aaaaaaatg ttttgtctgc agtttgttat 120  
 tgcatagtaa ataaaacctt ctctccagca caaaggcatg gaaattcagg aattacaatg 180  
 atgcggaaga aagcaaagtt ttccctcaga gagaatccag tg 222

<210> 20  
 <211> 73  
 <212> PRT  
 <213> H.Sapiens

<400> 20  
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 1 5 10 15  
 Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys  
 20 25 30  
 Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser  
 35 40 45  
 Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys  
 50 55 60  
 Ala Lys Phe Ser Leu Arg Glu Asn Pro  
 65 70

<210> 21  
 <211> 447  
 <212> DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 21

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tatctggtga ccaggatcac cacatagaat aggaaccgtg aggtacatgt ggatgtgcag      120
catggcactc acaaatttgc agaagggcag cccaaacatc caagtcttct tgatgaggta      180
ggtcaagcga aatggcactg tcagcagaaa aacgctgtgg accaccacca agttaatgac      240
cgccatggtg gtcactgacc ggggtgttcat tttcaccagg aggaaaagaa tggaaatgac      300
accaccagc cgcgaataa gcactatgaa gtagaggctg attaagtggg gtgtcactat      360
aggatcgcaa gaggaattcc tggaggtatt gtggccaggc atacttgga agtcacctgg      420
aggagaaaaa gcaccagagt aactgac                                         447

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&lt;210&gt; 22

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; H.Sapiens

&lt;400&gt; 22

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Val Ser Tyr Ser Gly Ala Phe Ser Pro Pro Gly Asp Phe Pro Ser Met
1           5           10           15
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
20           25           30
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
35           40           45
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
50           55           60
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
65           70           75           80
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
85           90           95
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
100          105          110
His Met Tyr Leu Thr Val Pro Ile Leu Cys Gly Asp Pro Gly His Gln
115          120          125
Ile Pro His Leu Leu Gln Val Gln Arg Gln Ser Gly Ile Leu Gln Lys
130          135          140
Thr Ala Cys Cys Gly
145

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&lt;210&gt; 23

&lt;211&gt; 222

<212> DNA  
<213> H.Sapiens

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agcgaacacg gtcagcagca ccagtccatt gcagagcacg gagagcaaca cgatggccca 180  
cacggccagg cggatgcccc agctttcaaa gaggtactca ca 222

<210> 24  
<211> 74  
<212> PRT  
<213> H.Sapiens

<400> 24  
Cys Glu Tyr Leu Phe Glu Ser Trp Gly Ile Arg Leu Ala Val Trp Ala  
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20 25 30  
Phe Ala Gly Gly Pro Ala Pro Leu Pro Pro Val Lys Phe Val Val Gly  
35 40 45  
Ala Ile Ala Gly Ala Asn Thr Leu Thr Gly Ile Ser Cys Gly Leu Leu  
50 55 60  
Ala Ser Val Asp Ala Leu Thr Leu Val Ser  
65 70

<210> 25  
<211> 246  
<212> DNA  
<213> H.Sapiens

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tgctgcggac gccactcctg cggcagagac ccgagtggct ccagcagtc ggcgagcgcg 120  
gctgaggctt ccgggggcct gcgcgctgc ctgccccggg gccttgatgg gagcttcagc 180  
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cccggt 246

<210> 26  
<211> 82  
<212> PRT  
<213> H.Sapiens

<400> 26



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 Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser  
 20 25 30  
 Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg  
 35 40 45  
 Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg  
 50 55 60  
 Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser  
 65 70 75 80  
 Pro Gly

<210> 27  
 <211> 420  
 <212> DNA  
 <213> H.Sapiens  
 <220>  
 <221> misc\_feature  
 <222> (81)..(106)  
 <223> n is any nucleic acid

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 cgcgatgcgg gcgtacatga ccacgatgag cgccagcggc gccaggtaga tgtgcgagaa 180  
 gagcacagtg gtgtagaccc tgcgcatgcc cttctcgggc caggcctccc agcaggagta 240  
 gagagggtag gagcggttgc gggcggtccac catgaagtgg tgctcctcac gggtgacggt 300  
 cagcgtgacg gccgagggac acatgatgag cagcgccagg gcccagatga cggcgatggt 360  
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<210> 28  
 <211> 139  
 <212> PRT  
 <213> H.Sapiens  
 <220>  
 <221> UNSURE  
 <222> (104)..(113)  
 <223> Xaa is Unknown

<400> 28  
 Phe Arg Cys Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys  
 Page 17

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Ala Leu Val Thr	Ile Ala Val Ile Trp	Ala Leu Ala Leu	Leu Ile Met
20	25	30	
Cys Pro Ser Ala	Val Thr Leu Thr	Val Thr Arg Glu	Glu His His Phe
35	40	45	
Met Val Asp Ala	Arg Asn Arg Ser Tyr	Pro Leu Tyr Ser	Cys Trp Glu
50	55	60	
Ala Trp Pro Glu	Lys Gly Met Arg	Arg Val Tyr Thr	Thr Val Leu Phe
65	70	75	80
Ser His Ile Tyr	Leu Ala Pro Leu	Ala Leu Ile Val	Val Met Tyr Ala
85	90	95	
Arg Ile Ala Arg	Lys Leu Cys Xaa	Xaa Xaa Xaa Xaa	Xaa Xaa Xaa
100	105	110	
Xaa Glu Ala Ala	Asp Pro Arg Ala	Ser Arg Arg Arg	Ala Arg Val Val
115	120	125	
His Met Leu Val	Met Val Ala Leu	Phe Phe Thr	
130	135		

<210> 29  
 <211> 318  
 <212> DNA  
 <213> H.Sapiens

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 tgggttgacg gcagcctggg cgaagctcat ccaaacagca gtggccaggt agcgggtggg 120  
 cacagcacag gctttcacia aactcgcca gtagcaggcc acgatgtagg gtgaccagag 180  
 gagcagaaaag agcagtgtga tcgcgtagaa catgcggccc agctgctttt cacccttgac 240  
 ctctccatg ccagtagcc gccggctggc tgcattgccc ttctgccgga taccagcag 300  
 ggttggtggc atgggccc 318

<210> 30  
 <211> 106  
 <212> PRT  
 <213> H.Sapiens

<400> 30

Gly Pro Met Pro	Pro Thr Leu Leu	Gly Ile Arg Gln	Asn Gly His Ala
1	5	10	15
Ala Ser Arg Arg	Leu Leu Gly Met	Asp Glu Val Lys	Gly Glu Lys Gln
20	25	30	
Leu Gly Arg Met	Phe Tyr Ala Ile	Thr Leu Leu Phe	Leu Leu Leu Trp

35                      40                      45  
 Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys  
 50                      55                      60  
 Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala  
 65                      70                      75                      80  
 Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu  
 85                      90                      95  
 Lys Lys Cys Leu Arg Thr His Ala Pro Cys  
 100                      105

<210> 31  
 <211> 354  
 <212> DNA  
 <213> H.Sapiens

<400> 31  
 tattctgttaa tgaagaatgt cattcacact gccattggca catccagtgg cctcacctag 60  
 cattgtgaaa gcccttcggt tgggtgtattg ccacttcatt ttaaaaggat gcacaagtcc 120  
 ctggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacia cagcggtaga 180  
 ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatc 240  
 atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgtaattat cactatcagt 300  
 ccattctgag cctctgcaa aaagtttgat aattgtaatt actctgtaga caca 354

<210> 32  
 <211> 117  
 <212> PRT  
 <213> H.Sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu  
 1                      5                      10                      15  
 Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu  
 20                      25                      30  
 Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe  
 35                      40                      45  
 Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu  
 50                      55                      60  
 Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val  
 65                      70                      75                      80  
 His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr  
 85                      90                      95  
 Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile

100 105 110

Leu His Tyr Arg Ile  
115

<210> 33  
<211> 621  
<212> DNA  
<213> H.Sapiens

<400> 33  
gagcaacatg atctttttga agtacttgac ggtgtcggtc ttgacgggtca cgaagcacag 60  
agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagtgaggta 120  
gtgctttctcc ttcacaaaca cgggtggggaa gaagtcgcgc acgatgggtga agccgtagaa 180  
gggcgcccag catagcacgt aggcggtgag gatgcacatg agcaccagga ccgtcttcct 240  
gcggcagcgc agcctcttgc ggatctgctc tgtctggaat ccagggaccg ccttgaacca 300  
gagctcccgg gagatcctgg catagcacag ggtcatgggtg accacggggc ccacgaattc 360  
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420  
ctggccgcag aagatctttt cctggctctt gacaatgacg aggaccgtct cggtggtgaa 480  
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540  
ggctgttttg cacttcattc gtggtctcag cggatggaca atagccagat acctagggca 600  
agaacacaag tggaggcagc c 621

<210> 34  
<211> 207  
<212> PRT  
<213> H.Sapiens

<400> 34

Gly Cys Leu His Leu Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His  
1 5 10 15  
Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala  
20 25 30  
Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe  
35 40 45  
Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe  
50 55 60  
Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr  
65 70 75 80  
Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met  
85 90 95

Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val  
 100 105 110  
 Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg  
 115 120 125  
 Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys  
 130 135 140  
 Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr  
 145 150 155 160  
 Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu  
 165 170 175  
 Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr  
 180 185 190  
 Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu  
 195 200 205

<210> 35  
 <211> 483  
 <212> DNA  
 <213> H.Sapiens

<400> 35  
 cagccacact gcagtgatga aatcaaagt ccaacaccaa ccatagtcac cattactaac 60  
 taagaagcca caaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120  
 ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180  
 gacagacagg cagcactcag tactgatggc actcagcatg ctcaggccta caaggtaggc 240  
 aaaggtcatc acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300  
 actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggccccggc 360  
 caggctgagg acgtagacag agaaggcggt cctgcgcagc cggaagccca ggagccagag 420  
 cacaaacccg ttctctacca gcccgaccag ggcaatgaaa aggatcagga agaccgggat 480  
 cag 483

<210> 36  
 <211> 161  
 <212> PRT  
 <213> H.Sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val  
 1 5 10 15  
 Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn  
 20 25 30

Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe  
 35 40 45  
 Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe  
 50 55 60  
 Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr  
 65 70 75 80  
 Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu  
 85 90 95  
 Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro  
 100 105 110  
 Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu  
 115 120 125  
 Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn  
 130 135 140  
 Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp  
 145 150 155 160

Leu

<210> 37  
 <211> 330  
 <212> DNA  
 <213> H.Sapiens

<400> 37  
 gagagtctga ttctgactta catcacatat gtaggcctgg gcatttctat ttgcagcctg 60  
 atcctttgct tgtccgttga ggctcctagtc tggagccaag tgacaaagac agagatcacc 120  
 tatttacgcc atgtgtgcat tgtaacatt gcagccactt tgctgatggc agatgtgtgg 180  
 ttcatgtgg cttcctttct tagtggccca ataacacacc acaagggatg tgtggcagcc 240  
 acattttttg gtcattttct ttacctttct gtatttttct ggatgcttgc caaggcactc 300  
 cttatcctct atggaatcat gattgttttc 330

<210> 38  
 <211> 110  
 <212> PRT  
 <213> H.Sapiens

<400> 38  
 Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser  
 1 5 10 15  
 Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser  
 20 25 30

Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val  
 35 40 45  
 Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala  
 50 55 60  
 Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala  
 65 70 75 80  
 Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu  
 85 90 95  
 Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe  
 100 105 110

<210> 39  
 <211> 628  
 <212> DNA  
 <213> H.Sapiens

<400> 39  
 ttgtgtggca gtagagagat gtcaggcttc agagtcaaca agaactggat ttcaaactgg 60  
 atttgaggac cccacacctt ggtaagtgac ttattatctg cgagcctctg tttctctctt 120  
 ctttaaataa ggacagtaaa tcccatcacg cagggtggtg gggagaatca gagatgatac 180  
 agctggtgat cacatctggt ttgtgttccc aggggcacca gactaggggt tctgagcatg 240  
 gatccaaccg tcccagtctt cggtacaaaa ctgacaccaa tcaacggacg tgaggagact 300  
 ccttgctaca atcagaccct gagcttcacg gtgctgacgt gcatcatttc ccttgctcga 360  
 ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgcag gaacgctgtc 420  
 tccatctaca tcctcaacct ggccgcagca gacttctctt tcctcagctt ccagattata 480  
 cgttcgccat tacgcctcat caatatcagc catctcatcc gcaaaatcct cgtttctgtg 540  
 atgacctttc cctactttac aggcctgagt atgctgagcg ccatcagcac cgagcgctgc 600  
 ctgtctgttc tgtggcccat ctggtacc 628

<210> 40  
 <211> 205  
 <212> PRT  
 <213> H.Sapiens

<400> 40

Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp  
 1 5 10 15  
 Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser  
 20 25 30  
 Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg  
 35 40 45

Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys  
 50 55 60  
 Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val  
 65 70 75 80  
 Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr  
 85 90 95  
 Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile  
 100 105 110  
 Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly  
 115 120 125  
 Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala  
 130 135 140  
 Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu  
 145 150 155 160  
 Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val  
 165 170 175  
 Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser  
 180 185 190  
 Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr  
 195 200 205

<210> 41  
 <211> 319  
 <212> DNA  
 <213> H.Sapiens

<400> 41  
 acagaaagca aggccaccag gaccttaggc atagtcattgg gagtggttgt gttgtgctgg 60  
 ctgcccttct ttgtcttgac gatcacagat cctttcatta attttacaac ccttgaagat 120  
 ctgtacaatg tcttctctctg gctaggctat ttcaactctg ctttcaatcc cattttatat 180  
 ggcattgcttt atccttggtt tcgcaaggca ttgaggtatga ttgtcacagg catgatcttc 240  
 caccctgact cttccaccct aagcctgttt tctgcccattg cttaggctgt gttcatcatt 300  
 caataggact cttttcttg 319

<210> 42  
 <211> 103  
 <212> PRT  
 <213> H.Sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe  
 1 5 10 15



Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe  
 20 25 30  
 Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu  
 35 40 45  
 Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr  
 50 55 60  
 Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe  
 65 70 75 80  
 His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val  
 85 90 95  
 Phe Ile Ile Gln Asp Ser Phe  
 100

<210> 43  
 <211> 515  
 <212> DNA  
 <213> H.Sapiens

<400> 43  
 taggaatctc agagaagaaa gtaaggaacc agaaaaccat aaaagaatgt aaatggaaaa 60  
 gaatcagcaa atcttattca cttatcacta aatctaaaat atgtcaaaat acatgaagac 120  
 aacaaatgct ttagaacaac tggtgaatgt attgtcctac aacttggcat atgatcatgc 180  
 ttgcctctct atgtccaagt gtttattttt gcagttgacc ttaatttcaa gttagttttg 240  
 aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagttgtt 300  
 gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaaccat 360  
 tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420  
 aaaatctcat aaacataagg aggagttata aaattcatat aagcatcaat cactgcatca 480  
 acgaggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44  
 <211> 148  
 <212> PRT  
 <213> H.Sapiens

<400> 44

Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala  
 1 5 10 15  
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala  
 20 25 30  
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp  
 35 40 45

Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe  
 50 55 60  
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val  
 65 70 75 80  
 Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu  
 85 90 95  
 Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg  
 100 105 110  
 Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met  
 115 120 125  
 Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu  
 130 135 140

Ser Ser Cys Ile  
 145

<210> 45  
 <211> 726  
 <212> DNA  
 <213> H.Sapiens

<400> 45  
 ctggaaagag gtccctcgatc taccctctac gccgtccttg gttttggggc tgtgctggca 60  
 gcgtttggaa acttactggt catgattgct atccttcaact tctaacaact gcacacacct 120  
 acaaactttc tgattgcgct gctggcctgt gctgacttct tgggtgggagt cactgtgatg 180  
 cccttcagca cagtggagtc tgtggagagc tgttggtact ttggggacag ttactgtaaa 240  
 ttccatacat gttttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc 300  
 tctgttgata gatacattgc tggtactgat cctctgacct atccaaccaa gtttactgtg 360  
 tcagtttcag ggatatgcat tggtctttcc tgggtctttt ctgtcacata cagcttttgc 420  
 atctttttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt 480  
 gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc 540  
 tttataccca atgtcgccat ggtgtttata tacagtaaga tttttttggt ggccaagcat 600  
 caggctagga agatagaaag tacagccagc caagctcagt ccttctcaga gagttacaag 660  
 gaaagagtag caaaaagaga gagaaaggct gccaaaacct tgggaattgc tatggcagca 720  
 tttctt 726

<210> 46  
 <211> 241  
 <212> PRT  
 <213> H.Sapiens

&lt;400&gt; 46

Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly  
 1 5 10 15  
 Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu  
 20 25 30  
 His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala  
 35 40 45  
 Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val  
 50 55 60  
 Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe  
 65 70 75 80  
 His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu  
 85 90 95  
 Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr  
 100 105 110  
 Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu  
 115 120 125  
 Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly  
 130 135 140  
 Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val  
 145 150 155 160  
 Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe  
 165 170 175  
 Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys  
 180 185 190  
 Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala  
 195 200 205  
 Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys  
 210 215 220  
 Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe  
 225 230 235 240

Leu

&lt;210&gt; 47

&lt;211&gt; 660

&lt;212&gt; DNA

&lt;213&gt; H.Sapiens

&lt;400&gt; 47

aaccaggtgg ccttactcct aagaccctg gccttgtcta tggcctttat caacagctgt

60

ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120  
 ctgctagctg ccttagaacg ggcacttagc gaggagccag atagtgcctg aatcccagct 180  
 cccaggcaga tgagtccttt ataacatgac ccaatttcct actccatttt cccaccactc 240  
 aatcctcttc ccaaacagct ctaccataat ccaacatcca acagaattta agagaataaa 300  
 ccacaacttt taa:tgagct ctatgtgcta ggtcatgttt tagaatacaa ccttaagtgc 360  
 ctggaagatg gaggcaagaa acaaacaagg tctcattctt tagaggaaga cagttcacca 420  
 agactcaaac agaaaaaaag atagttatct tgtgacaaaa caagtcataa aattgggtca 480  
 ggacctgcag caatgacttt atgctagaat ccagagcact agcaggaaac tgcttaaatt 540  
 ttacttaatc aaagtcaagt ttggacatac atgtcaggta aaacctagca gagatgagct 600  
 accttgattt taaaacttca agggatagct caatgtcatc aagatccttt tgatgacttg 660

<210> 48  
 <211> 211  
 <212> PRT  
 <213> H.Sapiens

<400> 48

Asn Gln Val Ala Leu Leu Arg Pro Leu Ala Leu Ser Met Ala Phe  
 1 5 10 15  
 Ile Asn Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Ile Gly His Asp  
 20 25 30  
 Phe Trp Glu His Leu Leu His Ser Leu Leu Ala Ala Leu Glu Arg Ala  
 35 40 45  
 Leu Ser Glu Glu Pro Asp Ser Ala Ile Pro Ala Pro Arg Gln Met Ser  
 50 55 60  
 Pro Leu His Asp Pro Ile Ser Tyr Ser Ile Phe Pro Pro Leu Asn Pro  
 65 70 75 80  
 Leu Pro Lys Gln Leu Tyr His Asn Pro Thr Ser Asn Arg Ile Glu Asn  
 85 90 95  
 Lys Pro Gln Leu Leu Ser Glu Leu Tyr Val Leu Gly His Val Leu Glu  
 100 105 110  
 Tyr Asn Leu Lys Cys Leu Glu Asp Gly Gly Lys Lys Gln Thr Arg Ser  
 115 120 125  
 His Ser Leu Glu Glu Asp Ser Ser Pro Arg Leu Lys Gln Lys Lys Arg  
 130 135 140  
 Leu Ser Cys Asp Lys Thr Ser His Lys Ile Gly Ser Gly Pro Ala Ala  
 145 150 155 160  
 Met Thr Leu Cys Asn Pro Glu His Gln Glu Thr Ala Ile Leu Leu Asn

165 170 175

Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr  
 180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe  
 195 200 205

Asp Asp Leu  
 210

<210> 49  
 <211> 465  
 <212> DNA  
 <213> H.Sapiens

<400> 49  
 gcttggttcac ggccaccatc ctcaagctgt tgcgcacgga ggaggcgac ggccgggagc 60  
 agcggaggcg cgcggtgggc ctggccgagg tggctctgct ggctttgtc acctgcttcg 120  
 cccccaacaa ctctgtgtc ctggcgaca tctgagccg cctgttctac ggcaagagct 180  
 actaccacgt gtacaagtc acgctgtgtc tcagctgcct caacaactgt ctggaccctg 240  
 ttgtttatta ctttgcgtcc cgggaattcc agctgcgcct gcgggaatat ttgggctgcc 300  
 gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctcttctcc gccaggacca 360  
 cgtccgtgag ctccgaggcc ggtgcgcacc ctgaagggat ggaggagacc accaggcccg 420  
 gcctccagag gcaggagagt gtgttctgag tcccgggggc gcagc 465

<210> 50  
 <211> 160  
 <212> PRT  
 <213> H.Sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His  
 1 5 10 15

Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu  
 20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala  
 35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr  
 50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe  
 65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr  
 85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu  
 100 105 110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala  
 115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln  
 130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg  
 145 150 155 160

<210> 51  
 <211> 603  
 <212> DNA  
 <213> H.Sapiens

<400> 51  
 ttactttattc tgccctttat ccaactttta attccctttg ctattctcct gcctcatttt 60  
 ctggcctcat tttccctatt atcctgcctc acattgatca agggatgagg ctggcaggat 120  
 ccggaaccca cagggccccg tgggccatga gaggctcctg gacttgaacc tcaggacact 180  
 cccactctgg ctgccggcag ggatggaagc tggatgagca ggcaggagct ggcagtgggg 240  
 gtggagagcc ataggctatt ggggtggaca ggcttgggtg cctcatggga gctccccatg 300  
 ggagctgtgg ccccttgggg cctcttattt ctcacccag gctttcccgg gagaggttca 360  
 agtcagaaga tgccccaaag atccacgtgg ccctgggtgg cagcctgttc ctctgaatc 420  
 tggccttctt ggtcaatgtg gggagtggct caaaggggtc tgatgctgcc tgctgggccc 480  
 ggggggctgt cttccactac ttcctgctct gtgccttcac ctggatgggc cttgaagcct 540  
 tccacctcta cctgctcgtc gtcagggtct tcaacaccta cttcgggcac tacttctga 600  
 agc 603

<210> 52  
 <211> 198  
 <212> PRT  
 <213> H.Sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser  
 1 5 10 15

Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile  
 20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp  
 35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys  
 50 55 60

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly  
1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys  
20 25 30

Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser  
 35 40 45  
 Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser  
 50 55 60  
 Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile  
 65 70 75 80  
 Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val  
 85 90 95  
 Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn  
 100 105 110

<210> 55  
 <211> 586  
 <212> DNA  
 <213> H.Sapiens

<400> 55  
 cacatcttaa caagactgaa aaacattgat ttgttttttaa tttgaagagc aattttatttg 60  
 ctattcattc atagtcttac ttgatttttta aaaactcatt tcgcttggtta atttttaaagg 120  
 tatcctgaac ttcgtctatc caactgctta tatatgttca gaaaacaaat tcatgggttc 180  
 tgaactgttc tttaaaacct gaccagttac aataactttt attgctttcc taaaccatgg 240  
 gtaaaataaa gcataaatca aaggattcat ggctgagtta taataagcac accaacagca 300  
 tcataaatac aggcaggggt tataaagccc ataaaggcat caattaatga atcaatgcta 360  
 tatggtaacc atgaaatcat aaatgctacc actgtgaccc ccagggtttt agctgctttt 420  
 ctctctctcc tggccactct ggctttgtta ctctctgagg atgattctgt cttgctacca 480  
 gtattttcta tctttttcgc ctgtcgtcta gccacaagaa atatgttacc atacagaatt 540  
 atcataataa aggtaggtat aaagaaggat agaaaatctg tcaaca 586

<210> 56  
 <211> 190  
 <212> PRT  
 <213> H.Sapiens

<400> 56  
 Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile  
 1 5 10 15  
 Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile  
 20 25 30  
 Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala  
 35 40 45



Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr  
 50 55 60  
 Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu  
 65 70 75 80  
 Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile  
 85 90 95  
 Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr  
 100 105 110  
 Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr  
 115 120 125  
 Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu  
 130 135 140  
 His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser  
 145 150 155 160  
 Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys  
 165 170 175  
 Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val  
 180 185 190

<210> 57  
 <211> 976  
 <212> DNA  
 <213> H.Sapiens

<400> 57  
 tttgtggcaa ggagaccctg atcccgggtct tcctgatcct ttccattgcc ctgggtcgggc 60  
 tggtaggaaa cgggtttgtg ctctggctcc tgggcttccg catgcgcagg aacgccttct 120  
 ctgtctacgt cctcagcctg gccggggccg acttctctt cctctgcttc cagattataa 180  
 attgcctggt gtacctcagt aacttcttct gtccatctc catcaatttc cctagcttct 240  
 tcaccactgt gatgacctgt gcctaccttg caggcctgag catgctgagc accgtcagca 300  
 ccgagcgctg cctgtccgtc ctgtggccca tctggtatcg ctgccgccgc ccagacacc 360  
 tgtcagcggc cgtgtgtgtc ctgctctggg cctgtccct actgctgagc atcttggaag 420  
 ggaagtctg tggcttctta tttagtgatg gtgactctgg ttggtgtcag acatttgatt 480  
 tcatcactgc agcgtggctg atttttttat tcatggttct ctgtgggtcc agtctggccc 540  
 tgctggtcag gatcctctgt ggtccagggt gtctgccact gaccaggctg tacctgacca 600  
 tctgctcac agtgtgggtg tccctcctct gcggcctgcc ctttggcatt cagtggttcc 660  
 taatattatg gatctggaag gattctgatg tcttattttg tcatattcat ccagtttcag 720  
 ttgtcctgtc atctcttaac agcagtgcc accccatcat ttacttcttc gtgggctctt 780

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ttaggaagca gtggcggstg cagcaccoga tcctcaagct ggctctccag agggctctgc      840
aggacattgc tgaggtggat cacagtgaag gatgcttccg tcagggcacc cggagattca      900
aagaagcatt ctggtgtagg gatggacccc tctacttcca tcatatatat gtggctttga      960
gaggcaactt tgcccc                                          976

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<210> 58
<211> 324
<212> PRT
<213> H.Sapiens

<220>
<221> UNSURE
<222> (266)..(266)
<223> Xaa is Unknown

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<400> 58

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Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
1          5          10          15
Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
20          25          30
Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
35          40          45
Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
50          55          60
Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
65          70          75          80
Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
85          90          95
Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
100         105         110
Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
115         120         125
Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
130         135         140
Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
145         150         155         160
Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
165         170         175
Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
180         185         190
Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Ser Leu

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195					200					205					
Leu	Cys	Gly	Leu	Pro	Phe	Gly	Ile	Gln	Trp	Phe	Leu	Ile	Leu	Trp	Ile
210						215					220				
Trp	Lys	Asp	Ser	Asp	Val	Leu	Phe	Cys	His	Ile	His	Pro	Val	Ser	Val
225					230					235					240
Val	Leu	Ser	Ser	Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr	Phe	Phe
				245					250					255	
Val	Gly	Ser	Phe	Arg	Lys	Gln	Trp	Arg	Xaa	Gln	His	Pro	Ile	Leu	Lys
			260					265						270	
Leu	Ala	Leu	Gln	Arg	Ala	Leu	Gln	Asp	Ile	Ala	Glu	Val	Asp	His	Ser
		275					280					285			
Glu	Gly	Cys	Phe	Arg	Gln	Gly	Thr	Arg	Arg	Phe	Lys	Glu	Ala	Phe	Trp
	290					295					300				
Cys	Arg	Asp	Gly	Pro	Leu	Tyr	Phe	His	His	Ile	Tyr	Val	Ala	Leu	Arg
305					310					315					320
Gly Asn Phe Ala															

<210> 59  
 <211> 578  
 <212> DNA  
 <213> H.Sapiens

<400> 59  
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 gtaacagggt accaaagggtg ttcagagcag cataatgggtc tagaaacgat gtaagcttca 120  
 tggatctgat tctcaatgga acaactgatt gaaagcaggc tgagattcga tcttgaatga 180  
 ccctcaagat atggaagggt aaaaaacata cgtaaaatgc aaggagtagc agaattggta 240  
 gccttcgtgc tttctgctta aggcagctgt cagtttgcag tccatgggtc aaagtgtgga 300  
 taatcgtggt atagcaaagt gtcactatca ccaaggggag gcagaaagta cttgcagtca 360  
 aaatcagggt gtaccactta atagtattga gttcatccga actggtgagg tcgagacagg 420  
 ctgatctgtt ggtcctgttg gttgatgtga tcaagaaggt catcggaatg acagctacca 480  
 gtgaaatgat ccacaccaca gcacaggcta caactgcaca tcgagttttg tgaatggaaa 540  
 agcagctcat tgggtgaatg atcacacagt agcggaag 578

<210> 60  
 <211> 192  
 <212> PRT  
 <213> H.Sapiens

<400> 60

Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His  
 1 5 10 15  
 Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser  
 20 25 30  
 Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg  
 35 40 45  
 Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn  
 50 55 60  
 Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu  
 65 70 75 80  
 Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu  
 85 90 95  
 Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg  
 100 105 110  
 Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe  
 115 120 125  
 His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser  
 130 135 140  
 Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp  
 145 150 155 160  
 His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val  
 165 170 175  
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys  
 180 185 190

<210> 61  
 <211> 872  
 <212> DNA  
 <213> H.Sapiens

<400> 61  
 gggagggctc gtagacacac taaccctacc ctttctgttt cttcctcacc tttcctttcc 60  
 atctgtttct catggtctcc tgtctgtctc tctctctctc ccctctttct ctctcctcgc 120  
 tctttctcat cccctccatt tctgtgtcaa tctcaatcca tttatatcgg tggccacttt 180  
 tctatctctt tgttctatct ctctctctct ctctttccca ctttgtctct gcacgcctgt 240  
 tgtgtttttc tgccctgtctc tctcttgccc tcatctctct gtctctctct tgccctcacc 300  
 tctctgtctc tctgtgtctg tgtctccccc gctcattccc atttgacagt gcaatgtagc 360  
 aggacaactc atggagcccc cccgggcccc tcgagtaccg gactggctga cccctagagg 420  
 ttggcagtag cccctgaccc tcagtatggc caacactacc ggagagcctg aggaggtgag 480

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cggcgctctg tccccaccgt ccgcatcagc ttatgtgaag ctggtactgc tgggactgat      540
tatgtgcgtg agcctggcgg gtaacgccat cttgtccctg ctggtgctca aggagcgggc      600
cctgcacaag gctccttact acttcctgct ggacctgtgc ctggccgatg gcatacgctc      660
tgccgtctgc tccccctttg tgctggcttc tgtgcgccac ggctcttcat ggaccttcag      720
tgcaactcagc tgcaagattg tggcctttat ggccgtgctc ttttgcttcc atgcggcctt      780
catgctgttc tgcacacagc tcaccgccta catggccatc gccaccacc gcttctacgc      840
caagcgcgatg acactctgga catgcgcggc tg                                     872

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<210> 62  
 <211> 143  
 <212> PRT  
 <213> H.Sapiens

<400> 62

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Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1          5          10          15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
          20          25          30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
          35          40          45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
          50          55          60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
          65          70          75          80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
          85          90          95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
          100         105         110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
          115         120         125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Glu
          130         135         140

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<210> 63  
 <211> 962  
 <212> DNA  
 <213> H.Sapiens

<400> 63

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aaaaattgct gtactgaact attgaatgga acttggaat aaagtcctt caaaaataac      60
tattcttcaa cagagagtaa taggtaaatg ttttagaagt gagaggactc aaattgccaa      120

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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180  
 aaacatgaga aggaactgta acctgattat ggatttgga aaaagataaa tcaacacaca 240  
 aagggaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300  
 taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt 360  
 aatgggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatata 420  
 acacttcaaa caacttcata cccaacaaa ttggctcatt cattccatgg ccaactgtgga 480  
 ctttcttctg ggggtgtctgg tcatgcctta cagtatgggtg agatctgctg agcactgttg 540  
 gtattttgga gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc 600  
 ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660  
 gagatataaa gccaaagatga atatcttggg tatttgtgtg atgatcttca ttagttggag 720  
 tgtccctgct gtttttgcatt ttggaatgat ctttctggag ctaaacttca aaggcgctga 780  
 agagatatat tacaacatg ttcactgcag aggaggttgc tctgtcttct ttagcaaaat 840  
 atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt 900  
 ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagtg atgccaatca 960  
 ga 962

<210> 64  
 <211> 238  
 <212> PRT  
 <213> H.Sapiens

<400> 64

Arg Glu Lys Thr Asp Gln Pro Ser Gly Met Met Pro Phe Cys His Asn  
 1 5 10 15  
 Ile Ile Asn Ile Ser Cys Val Lys Asn Asn Trp Ser Asn Asp Val Arg  
 20 25 30  
 Ala Ser Leu Tyr Ser Leu Met Val Leu Ile Ile Leu Thr Thr Leu Val  
 35 40 45  
 Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu His  
 50 55 60  
 Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe Leu  
 65 70 75 80  
 Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu His  
 85 90 95  
 Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr Asp  
 100 105 110

Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser Ile  
 115 120 125  
 Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys Met  
 130 135 140  
 Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val Pro  
 145 150 155 160  
 Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys Gly  
 165 170 175  
 Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys Ser  
 180 185 190  
 Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser Phe  
 195 200 205  
 Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr Leu  
 210 215 220  
 Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln  
 225 230 235

<210> 65  
 <211> 1018  
 <212> DNA  
 <213> H.Sapiens

<400> 65  
 aacagtcccc ggtggaacct gggcatgtat attttgattg ttttatgcat actcctagtg 60  
 aagaaccaat gtcttgctca gatagaagca agatactcag acttagtttc tctgtagctc 120  
 ctgcttttta ttattcctgg ttggattgca ccactactca gtttctattt tataatactg 180  
 attataaaac atgggagggg aataactttg tattggtttt tatggataat ttattatgtg 240  
 tcctagactc tggccttgtc aaaagaagga cgtaagaagg cacgatgtat tatacttggg 300  
 aatgatagaa gagactgacc tggatatttc acccggaaga gggaaaggat tttaactaca 360  
 aatacaggaa tccagcagat ggcatcagag aacactataa aaaagaaacg atttgcaaca 420  
 gccacctctc ttccaaaaca attccttact tctgtggtct gcaaggcggg tttttgaatg 480  
 gaacagaaca tagtaatata ggaaaacaca atgatgagaa aagccagcaa gttcacacct 540  
 gttggggaaa agcacacttt taacatctca ggcgtaaaag tcaacagtaa aattactgtg 600  
 gtacagggtg agtatccctt acccaaaatg ttgaaaacca gaaatgtttt ggatttcgga 660  
 tttcggaata ttacacatt cataatgata tatcttggaa atggttccca agtctaaaca 720  
 caaaatttat ttatgtttca tatacacctt ataacatag tctgaaagta atttgtaca 780  
 atattttaaa taattttggg catgaaacaa agtttgcata cattgaacca tcagacagca 840  
 aaagcttcag gtgtggaatt ttccacttgg ggcatcatgt tgatgctcaa aaagttccat 900

atttttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960  
 gttaaataca gtgcctcttc cacgggcact ttcaggaagc attcttttat ataagccc 1018

<210> 66  
 <211> 327  
 <212> PRT  
 <213> H.Sapiens

<400> 66

Tyr Ile Lys Glu Cys Phe Leu Lys Val Pro Val Glu Glu Ala Leu Tyr  
 1 5 10 15  
 Leu Thr Ser Lys Tyr Arg Leu Ser Ile Cys Asn Leu Lys Ile Gln Asn  
 20 25 30  
 Leu Lys Cys Ser Lys Ile Trp Asn Phe Leu Ser Ile Asn Met Met Pro  
 35 40 45  
 Gln Val Glu Asn Ser Thr Pro Glu Ala Phe Ala Val Trp Phe Asn Val  
 50 55 60  
 Cys Lys Leu Cys Phe Met Pro Lys Ile Ile Asn Ile Val Gln Asn Tyr  
 65 70 75 80  
 Phe Gln Thr Met Cys Ile Arg Cys Ile Asn Ile Asn Lys Phe Cys Val  
 85 90 95  
 Thr Trp Glu Pro Phe Pro Arg Tyr Ile Ile Met Asn Val Ile Phe Arg  
 100 105 110  
 Asn Pro Lys Ser Lys Thr Phe Leu Val Ser Asn Ile Leu Gly Lys Gly  
 115 120 125  
 Tyr Ser Thr Cys Thr Thr Val Ile Leu Leu Leu Thr Phe Thr Pro Glu  
 130 135 140  
 Met Leu Lys Val Cys Phe Ser Pro Thr Gly Val Asn Leu Leu Ala Phe  
 145 150 155 160  
 Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys  
 165 170 175  
 Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val  
 180 185 190  
 Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys  
 195 200 205  
 Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu  
 210 215 220  
 Ile Pro Gly Gln Ser Leu Leu Ser Phe Pro Ser Ile Ile His Arg Ala  
 225 230 235 240  
 Phe Leu Arg Pro Ser Phe Asp Lys Ala Arg Val Asp Thr Ile Ile His



acaactccagc cagcatcgga tcccacagct cagccacagc tgaaccctac ggcccagcca 1140  
 cagtcggatc ccacagccca gccacagctg aacctcatgg cccagccaca gtcagattct 1200  
 gtggcccagc cacaggcaga cactaacgtc cagaccctg cacctgctgc c 1251

<210> 68  
 <211> 417  
 <212> PRT  
 <213> H.Sapiens  
 <400> 68

Thr	Thr	Met	Glu	Ala	Asp	Leu	Gly	Ala	Thr	Gly	His	Arg	Pro	Arg	Thr	
1				5					10					15		
Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly	Gly	Trp	Asp	Thr	Val	
			20					25					30			
Phe	Leu	Val	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Pro	Ala	Asn	Gly	Leu	Met	
		35					40					45				
Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly	Ala	Gly	Thr	Arg	Leu	
	50					55					60					
Ala	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	Phe	Leu	Phe	Leu	Ala	
65					70					75					80	
Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His	Trp	Pro	
			85					90					95			
Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly	Val	Ser	
			100					105					110			
Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp	Arg	Cys	
		115					120					125				
Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro	Val	Arg	
	130					135					140					
Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr	Leu	Phe	
145				150						155					160	
Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp	Tyr	Asp	
			165					170						175		
Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser	Leu	Arg	
			180					185					190			
Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu	Leu	Val	
		195					200					205				
Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His	Arg	Gln	
	210					215					220					
Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg	Thr	Ile	
225					230					235					240	

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu  
 245 250 255  
 Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
 260 265 270  
 Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
 275 280 285  
 Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
 290 295 300  
 Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
 305 310 315 320  
 Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
 325 330 335  
 Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
 340 345 350  
 Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
 355 360 365  
 Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
 370 375 380  
 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
 385 390 395 400  
 Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
 405 410 415

Ala

<210> 69  
 <211> 659  
 <212> DNA  
 <213> H.Sapiens

<400> 69  
 tacaggcctg agcatgctgg gctccatcag caccaagcac tgctgtcca tctgtggcc 60  
 catctagtac cgctgccacc accccacaca cctgtcagca gtcgtgtgtc ctgctctggg 120  
 ccctgtccct gctgcagagc atcctggaat ggatgttctg tggcttcctg tctagtgggtg 180  
 ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg atttttttat 240  
 gtgtggttct ctgcggttcc agcccgggtc tgctggtcag gatcctttgt ggatcccgga 300  
 agatgccctt gaccaggctg tacatgacca tctgtctcag agtgctgggtc ttctctctct 360  
 gtgacctgcc ctttggcatt cagtgattcc tatttttctg gatccacgtg gatttgtcac 420  
 gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaccc cattatttac 480  
 ttcttcatgg gctcctttag gcagcttcaa aacaggaaga ctctctagct ggttctccag 540

agggctctgc aggcacagcc tgagggtggaa gaaggcagat ggcggctttc tgaggaaacc 600  
 ctggagctgt catgaagcag attggggcca tgaggaagag cctctgccct gtcagtcag 659

<210> 70  
 <211> 213  
 <212> PRT  
 <213> H.Sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val  
 1 5 10 15  
 His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val  
 20 25 30  
 Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser  
 35 40 45  
 Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe  
 50 55 60  
 Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val  
 65 70 75 80  
 Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val  
 85 90 95  
 Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys  
 100 105 110  
 Trp Ser Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr  
 115 120 125  
 Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe  
 130 135 140  
 Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met  
 145 150 155 160  
 Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln  
 165 170 175  
 Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu  
 180 185 190  
 Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala  
 195 200 205  
 Ser Ala Leu Ser Val  
 210

<210> 71  
 <211> 559  
 <212> DNA  
 <213> H.Sapiens

<400> 71  
 atgccgaagg caggccgcag aagagaagag gaggacggtg aggaggatga gcccagggaa 60  
 gccccgggggt gggggccgct gggggcctcg ctccacccgc agcagcagca taaggctggc 120  
 cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgtccg 180  
 gcacaagtgg cggc:gggct ccccgaagaa ctgggtgcag gcgccgctga gcagcaggtg 240  
 cagcagcagg cagagggccc aggtgagggc gcacacacag gtggtcaggt ggcgtgggcg 300  
 gcggcacagag taccaggctg ggaagagggc ggccaggcac tgctccacgc tgacggccgc 360  
 caggagactc aggcccacga tgtagcagaa gaagcgcagc gttgccaggc tggctcgcac 420  
 gaagcccggg aagtccagcc ggccttgag caagtcgggg acgatggcca ccatgtggca 480  
 gccaaaggaag atgagatccg cgcaggccac gtccaggagg tagatggcga aagggtttct 540  
 gtagacattg gagctgagc 559

<210> 72  
 <211> 211  
 <212> PRT  
 <213> H.Sapiens

<400> 72

Leu	Ser	Ser	Asn	Val	Tyr	Arg	Asn	Pro	Phe	Ala	Ile	Tyr	Leu	Leu	Asp
1				5					10				15		
Val	Ala	Cys	Ala	Asp	Leu	Ile	Phe	Leu	Gly	Cys	His	Met	Val	Ala	Ile
			20					25					30		
Val	Pro	Asp	Leu	Leu	Gln	Gly	Arg	Leu	Asp	Phe	Pro	Gly	Phe	Val	Gln
			35				40					45			
Thr	Ser	Leu	Ala	Thr	Leu	Arg	Phe	Phe	Cys	Tyr	Ile	Val	Gly	Leu	Ser
	50					55					60				
Leu	Leu	Ala	Ala	Val	Ser	Val	Glu	Gln	Cys	Leu	Ala	Ala	Leu	Phe	Pro
65					70				75						80
Ala	Trp	Tyr	Ser	Cys	Arg	Arg	Pro	Arg	His	Leu	Thr	Thr	Cys	Val	Cys
				85					90					95	
Ala	Leu	Thr	Trp	Ala	Leu	Cys	Leu	Leu	Leu	His	Leu	Thr	Thr	Cys	Val
			100				105						110		
Cys	Ala	Leu	Thr	Trp	Ala	Leu	Cys	Leu	Leu	Leu	His	Leu	Leu	Leu	Ser
		115					120					125			
Gly	Ala	Cys	Thr	Leu	Leu	Leu	Ser	Gly	Ala	Cys	Thr	Gln	Phe	Phe	Gly
	130						135				140				
Glu	Pro	Ser	Arg	His	Leu	Cys	Arg	Thr	Leu	Trp	Leu	Val	Ala	Ala	Val
145					150					155					160

Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu  
                   165                                  170                                  175  
 Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe  
                   180                                  185                                  190  
 Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys  
                   195                                  200                                  205  
 Leu Arg His  
                   210

<210> 73  
 <211> 1008  
 <212> DNA  
 <213> H.Sapiens

<400> 73  
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 actaacacac tagtggctgt ggctgtgctg ctgttgatcc acaagaatga tgggtgtcagt 120  
 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttggtgtggc catctctggc 180  
 ctactcacag accagctctc cagcccttct cggcccacac agaagacct gtgcagcctg 240  
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacggtcac gctgatcacc 300  
 tttgacaggt accttgccat caagcagccc ttcogctact tgaagatcat gagtgggttc 360  
 gtggccgggg cctgcattgc cgggctgtgg ttagtgtctt acctcattgg ctctctccca 420  
 ctcggaatcc ccatgttcca gcagactgcc taaaaagggc agtgcagctt ctttgctgta 480  
 tttcaccttc acttcgtgct gacctctctc tgcgttggct tcttcccage catgctcctc 540  
 tttgtcttct tctactgcga catgctcaag attgcctcca tgcacagcca gcagattcga 600  
 aagatggaac atgcaggagc catggctgga gggttatcga cccacaggac tcccagcgac 660  
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 ttccttatca ctggcattgt gcaggtggcc tgccaggagt gtcacctcta cctagtgtgtg 780  
 gaacggtacc tgtggctgct cggcgtgggc aactccctgc tcaaccact catctatgcc 840  
 tattggcaga aggaggtgcg actgcagctc taccacatgg ccctaggagt gaagaaggtg 900  
 ctcacctcat tctctctctt tctctcggcc aggaattgtg gccagagag gccagggaa 960  
 agttcctgtc acatcgtcac tatctccage tcagagtttg atggctaa 1008

<210> 74  
 <211> 335  
 <212> PRT  
 <213> H.Sapiens

&lt;400&gt; 74

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser  
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 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu  
 20 25 30  
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
 35 40 45  
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
 50 55 60  
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
 65 70 75 80  
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
 85 90 95  
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
 100 105 110  
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
 115 120 125  
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
 130 135 140  
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
 145 150 155 160  
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
 165 170 175  
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala  
 180 185 190  
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
 195 200 205  
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
 210 215 220  
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240  
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
 245 250 255  
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270  
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285  
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
325 330 335

<210> 75  
<211> 2137  
<212> DNA  
<213> H.Sapiens

<400> 75  
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aagcgttgca tcctgttacc tggagaccct ctgagctctc acctgctact tctgccgtg 180  
cttctgcaca gagcccgggc gaggaccctt ccaggatgca ggtcccgaac agcaccggcc 240  
cggacaacgc gacgtgcag atgctgcgga acccggcgat cgcggtggcc ctgcccgtag 300  
tgtactcgct ggtggcgggc gtcagcatcc cgggcaacct cttctctctg tgggtgctgt 360  
gccggcgcat ggggccaga tcccgcgtcg tcatcttcat gatcaacctg agcgtcacgg 420  
acctgatgct ggccagcgtg ttgcctttcc aaatctacta ccattgcaac cgccaccact 480  
gggtattcgg ggtgctgctt tgcaacgtgg tgaccgtggc cttttacgca aacatgtatt 540  
ccagcatcct caccatgacc tgtatcagcg tggagcgtt cctgggggtc ctgtaccgcg 600  
tcagctcaa gcgctggcg cgccgtcggt acgcggtggc cgcgtgtgca gggacctggc 660  
tgctgctcct gaccgcctg tcccgcgtgg cgcgcaccga tctcacctac ccggtgcaog 720  
ccctgggcat catcacctgc ttgcagctcc tcaagtggac gatgctcccc agcgtggcca 780  
tgtggggcgt gttcctcttc accatcttca tcctgtgtt cctcatcccg ttctgatca 840  
ccgtggcttg ttacacggc accatcctca agctgttgcg cacggaggag gcgcacggcc 900  
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gcttcgcccc caacaacttc gtgctcctgg cgcacatcgt gagccgcctg ttctacggca 1020  
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acctgtttgt ttattacttt gcgtcccggg aattccagct gcgcctgcgg gaatatttgg 1140  
gctgccgcgg ggtgccaga gacaccctgg acacgcgcgg cgagagcctc ttctccgcca 1200  
ggaccacgtc cgtgcgctcc gaggccggtg cgcaccctga agggatggag ggagccacca 1260  
ggccccgcct ccagaggcag gagagtgtgt tctgagctcc gggggcgag cttggagagc 1320  
cgggggcgca gcttgaggga tccagggcg catggagagg ccacggtgcc agaggttcag 1380  
ggagaacagc tgcgttgctc ccaggcactg cagaggcccg gtggggaagg gtctccaggc 1440

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tttattcctc ccaggcactg cagaggcacc ggtgaggaag ggtctccagg cttcactcag 1500
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acacctgtcc ataccggagg atggatattc aaccagcccc accgcctacc cgactcggtt 1860
tctggatata ctctgtgggc gaactgcgag cccattccc agctcttctc cctgctgaca 1920
tcgtccctta gttgtggttc tggccttctc cattctctc caggggttct ggtctccgta 1980
gcccgggtgca cgccgaaatt tctgtttatt tcaactcagg gcaactgtgg tgctgtggtt 2040
ggaattcttc tttcagagga gcgcctgggg ctctgcaag tcagctactc tccgtgccca 2100
cttccctca cacacacacc cccctcgtgc cgaattc 2137

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<210> 76  
 <211> 359  
 <212> PRT  
 <213> H.Sapiens

<400> 76

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Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
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Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
35        40        45
Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
50        55        60
Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65        70        75        80
Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
85        90        95
Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
100       105       110
Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
115      120      125
Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
130      135      140

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Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg  
 145 150 155 160  
 Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
 165 170 175  
 Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
 180 185 190  
 Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
 195 200 205  
 Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
 210 215 220  
 Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
 225 230 235 240  
 Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
 245 250 255  
 Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
 260 265 270  
 His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
 275 280 285  
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
 290 295 300  
 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
 305 310 315 320  
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
 325 330 335  
 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
 340 345 350  
 Gln Arg Gln Glu Ser Val Phe  
 355

<210> 77  
 <211> 1197  
 <212> DNA  
 <213> H.Sapiens

<400> 77  
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 gtggtgtgcc tggcgggtgtg cgccttcac gtgctagaga atctagccgt gttgttggtg 180  
 ctcggacgcc accgcgcgtt ccaagctccc atgttctgct tcttgggcag cctcacgttg 240  
 tcggatctgc tggcaggcgc cgcctacgcc gccaacatcc tactgtcggg gccgctcacg 300

ctgaaactgt cccccgcgt ctggttcgca cgggagggag gcgtcttcgt ggcactcact 360  
 gcgtccgtgc tgagcctcct ggccatcgcg ctggagcgca gcctcaccat ggcgcgcagg 420  
 gggcccgcgc ccgtctccag tcggggggcg acgctggcga tggcagccgc ggcctggggc 480  
 gtgtcgctgc tctcggggt cctgccagcg ctgggctgga attgcctggg tcgcctggac 540  
 gcttgctcca ctgtcttgcc gctctacgcc aaggcctacg tgctcttctg cgtgctcgcc 600  
 ttcgtgggca tcttgccgc tatctgtgca ctctacgcgc gcatctactg ccaggtagcg 660  
 gccaacgcgc ggcgcctgcc ggcacggccc gggactgcgg ggaccacctc gaccgcggcg 720  
 cgctcgcaagc cgcgctcgct ggccttgctg cgcacgctca gcgtggtgct cctggccttt 780  
 gtggcatgtt ggggccccct ctctctgctg ctgttgctcg acgtggcgtg cccggcgcg 840  
 acctgtcctg tactcctgca ggccgatccc ttctgggac tggccatggc caactcactt 900  
 ctgaacccca tcatctacac gctcaccaac cgcgacctgc gccacgcgct cctgcgcctg 960  
 gtctgctgcg gacgccactc ctgcggcaga gaccgcagtg gctcccagca gtcggcgagc 1020  
 gcggctgagg ctccggggg cctgcgcgcg tgctgcccc cgggccttga tgggagcttc 1080  
 agcggctcgg agcgtcatc gccccagcg gacgggctgg acaccagcgg ctccacaggc 1140  
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<210> 78  
 <211> 398  
 <212> PRT  
 <213> H.Sapiens

<400> 78

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val  
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 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro  
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 Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala  
 35 40 45  
 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His  
 50 55 60  
 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu  
 65 70 75 80  
 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser  
 85 90 95  
 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu  
 100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala  
 115 120 125  
 Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro  
 130 135 140  
 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly  
 145 150 155 160  
 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu  
 165 170 175  
 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala  
 180 185 190  
 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile  
 195 200 205  
 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg  
 210 215 220  
 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala  
 225 230 235 240  
 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val  
 245 250 255  
 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu  
 260 265 270  
 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala  
 275 280 285  
 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile  
 290 295 300  
 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu  
 305 310 315 320  
 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln  
 325 330 335  
 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu  
 340 345 350  
 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro  
 355 360 365  
 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala  
 370 375 380  
 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp  
 385 390 395

<210> 79  
 <211> 1041  
 <212> DNA  
 <213> H.Sapiens

<400> 79  
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 tgcttcacaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180  
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 ttcacatcatg tgggtggcaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga 720  
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 cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 840  
 tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900  
 cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960  
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 cacattgttg agtggcactg a 1041

<210> 80  
 <211> 346  
 <212> PRT  
 <213> H.Sapiens

<400> 80

Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln  
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 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly  
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 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys  
 35 40 45  
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu  
 50 55 60  
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His  
 65 70 75 80

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
                     85                    90                    95  
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp  
                     100                    105                    110  
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
                     115                    120                    125  
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
                     130                    135                    140  
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu  
                     145                    150                    155                    160  
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp  
                     165                    170                    175  
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
                     180                    185                    190  
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln  
                     195                    200                    205  
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val  
                     210                    215                    220  
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
                     225                    230                    235                    240  
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val  
                     245                    250                    255  
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
                     260                    265                    270  
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
                     275                    280                    285  
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
                     290                    295                    300  
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
                     305                    310                    315                    320  
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly  
                     325                    330                    335  
 Gln Trp Asp Pro His Ile Val Glu Trp His  
                     340                    345

<210> 81  
 <211> 2525  
 <212> DNA  
 <213> H.Sapiens

<400> 81  
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60

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tggtgggtgt catttccatt cttttcctcc tggtgaaaat gaacacccgg tcagtgacca	180
ccatggcgggt cattaacttg gtggtggtcc acagcgtttt tctgctgaca gtgccatttc	240
gcttgacctt cctcatcaag aagacttgga tgtttgggct gcccttcgc aaatttgatga	300
gtgccatgct gcacatccac atgtacctca cgttcctatt ctatgtggtg atcctgggtca	360
ccagatacct catcttcttc aagtgcacaa acaaagtggga attctacaga aaactgcatg	420
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tctcccggtt tggaatccat gaggaatata atgaggagca ctgttttaaa tttcacaag	540
agcttgctta cacatatgtg aaaatcatca actatatgat agtcattttt gtcatagccg	600
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gccactcttt actatccac caggagttct gggctcagct gaaaaacctt ttttttatag	720
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taacagcaat tagctgctat gatttgcttc tctttgtctt tgggggaagc cattgggtta	900
agcaaaagat aattggctta tggaaattgtg ttttgtgccg ttagccacaa actacagtat	960
tcatatttgc ttcttttata ttgggaataa aaatgggtat aggggaggta agaatggtat	1020
ttcattactt gatcaaaacc atgccttgat gtacccaaaa caaaaggact ataaaatgca	1080
agagccctca ttgtagtctt tatgggatcc ctcccatctc tgagtgatgg ccgtacaaag	1140
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ctgtgtggcc catgaaagca acatagggtt taagagtttt agagtttcat tagctcattc	1260
taagttcctc tgtttgaagc atgggtctctt aggttttgga ctgaactcag acctttagtt	1320
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caaactctcc ttcgctaacc aggttagatg tccattcat ctcatgccct gataaaaact	1440
gataagggga gagaatagtt aaaaattttt ctagggtatc ataactctgg taggaagtca	1500
tctgtctaga aatcaagaga aaaagaacgt gtggcctcct gttataacaa gggtttctag	1560
atttgtcctg tgaaaggctg tttaaggact tggggatcaa cttcctcaat tatcaccaat	1620
tgcactgttg ctccaaaaat catttaaaag cttactggac atatctacat aatggtgaaa	1680
ctgtaattta gagactatcc ctgactaatg tgctggtagg cattaaaatg agttcccaag	1740
ggaagtgatt aaaaattttt tctcttctgt tttttgagag aatttctaga tgtcctgggc	1800

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cacagttaat taagattttt aggggggaca gaaagttata ctgaaatctt tagagctccc 1860
ttccgccgtt aaaattatat atatatatat ttaaattata ccttaagttc tgggggtacat 1920
gtgcagaatg tgcaggtttg ttacataggt atacacgtgc catggtgggt tgcggcacct 1980
gtcaacccat ctacattagg tattttctct aatgctctcc ctcccctagc cccccacccc 2040
tggacaggcc ccattgtgtg atgttcccct ccctgtgtcc atgtgttttc attgttcaac 2100
tcccacttct aagtgagaac atgcggtgtt tggttttctg ttctgtgtt agtttgtga 2160
gaatgatggt ttccaggtta aaattatata tttttaaata aatgaaaact gtgtttttaa 2220
aagaggactt ttgagaagta tatagaaaaa ccattaattt agactctgtg agattaggtt 2280
gcatgaagaa ggttttctga atatttgaag agtggataaa taaatgtccc ccaaagcaat 2340
aaaatcataa tcctttaaaa tataggaaaa ataactaatg ggaactaggc ttaatactcg 2400
ggatgaaata atctgtacaa caaactccca tgacacatgt ttacctatgt aacaaacctg 2460
cacatgtacc cctgaactta aaataaaatt taaagtataa taataaaata atatggattt 2520
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<210> 82
<211> 312
<212> PRT
<213> H.Sapiens

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<400> 82

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Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn
1          5          10          15
Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe
      20          25          30
Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu
      35          40          45
Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn
      50          55          60
Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu
65          70          75          80
Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys
      85          90          95
Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe
      100         105         110
Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys
      115         120         125
Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala

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130                      135                      140  
 Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser  
 145                      150                      155                      160  
 Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe  
                     165                      170                      175  
 His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile  
                     180                      185                      190  
 Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val  
                     195                      200                      205  
 Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser  
                     210                      215                      220  
 His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val  
 225                      230                      235                      240  
 Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu  
                     245                      250                      255  
 Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr  
                     260                      265                      270  
 Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu  
                     275                      280                      285  
 Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly  
                     290                      295                      300  
 Leu Trp Asn Cys Val Leu Cys Arg  
 305                      310

<210> 83  
 <211> 1125  
 <212> DNA  
 <213> H.Sapiens

<400> 83  
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 cagctgtgct acgcgaacgt gaatgggtcc tgtgtgaaaa tccccttctc gccgggatcc 180  
 cgggtgattc tgtacatagt gtttggcttt ggggctgtgc tggctgtgtt tggaaacctc 240  
 ctggtgatga tttcaatcct ccatttcaag cagctgcaact ctccgaccaa ttttctcggt 300  
 gcctctctgg cctgcgctga tttcttggtg ggtgtgactg tgatgccctt cagcatggtc 360  
 aggacgggtg agagctgctg gtattttggg aggagttttt gtactttcca cacctgctgt 420  
 gatgtggcat tttgttactc ttctctcttt cacttgctgt tcacttccat cgacaggtac 480  
 attgcggtta ctgacccccct ggtctatcct accaagttca ccgtatctgt gtcaggaatt 540



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tgcacacagcg tgcctggat cctgcccctc atgtacacagcg gtgctgtgtt ctacacaggt      600
gtctatgacg atgggctgga ggaattatct gatgccctaa actgtatagg aggttgtcag      660
accgttgtaa atcaaaactg ggtgttgaca gattttctat ccttctttat acctaccttt      720
attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata      780
gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg      840
agagagagaa aagcagctaa aaccctgggg gtcacagtgg tagcatttat gatttcatgg      900
ttaccatata gcattgattc attaatgat gcctttatgg gctttataac ccctgcctgt      960
atztatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat     1020
gctttatttt acccatgggt taggaaagca ataaaagtta ttgtaactgg tcaggtttta     1080
aagaacagtt cagcaacat gaatttggtt tctgaacata tataa                        1125

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<210> 84  
 <211> 345  
 <212> PRT  
 <213> H.Sapiens

<400> 84

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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1          5          10          15
Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
20          25          30
Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
35          40          45
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
50          55          60
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65          70          75          80
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
85          90          95
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
100         105         110
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
115         120         125
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
130         135         140
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145         150         155         160
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly

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<210> 85
<211> 1020
<212> DNA
<213> H.Sapiens
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<400> 85						
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tatggcatta	tcttcctcgt	gggatttcca	ggcaatgcag	tagtgatatc	cacttacatt	180
ttcaaaatga	gaccttgga	gagcagcacc	atcattatgc	tgaacctggc	ctgcacagat	240
ctgctgtatc	tgaccagcct	ccccttcctg	attcaactact	atgccagtg	cgaaaactgg	300
atctttggag	atttcatgtg	taagtttata	cgcttcagct	tccatttcaa	cctgtatagc	360
agcatcctct	tcctcacctg	tttcagcatc	ttccgctact	gtgtgatcat	tcacccaatg	420
agctgctttt	ccattcacaa	aactcgatgt	gcagttgtag	cctgtgctgt	ggtgtggatc	480
atttcaactg	tagctgtcat	tcggatgacc	ttcttgatca	catcaaccaa	caggaccaac	540

agatcagcct gtctcgacct caccagttcg gatgaactca atactattaa gtggtacaac 600  
 ctgattttga ctgcaagtac tttctgcctc cccttggtga tagtgacact ttgctatacc 660  
 acgattatcc acactttgac ccatggactg caaactgaca gctgccttaa gcagaaagca 720  
 cgaaggctaa ccattctgct actccttgca ttttacgtat gttttttacc cttccatata 780  
 ttgaggggtca ttcaggatcg aatctcagcc tgctttcaat cagttgttcc attgagaatc 840  
 agatccatga agcttacatc gtttctagac cattatgctg ctctgaacac ctttggtaac 900  
 ctgttactat atgtgggtgg cagcgacaac tttcagcagg ctgtctgctc aacagtgaga 960  
 tgcaaagtaa gcgggaacct tgagcaagca aagaaaatta gttactcaaa caacccttga 1020

<210> 86  
 <211> 336  
 <212> PRT  
 <213> H.Sapiens

<400> 86

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Tyr	Ala	Ala	Ala	Phe	Gly	Asn	Cys	Thr	Asp	Glu	Asn	Ile	Pro	Leu	Lys
			20					25					30		
Met	His	Tyr	Leu	Pro	Val	Ile	Tyr	Gly	Ile	Ile	Phe	Leu	Val	Gly	Phe
		35				40					45				
Pro	Gly	Asn	Ala	Val	Val	Ile	Ser	Thr	Tyr	Ile	Phe	Lys	Met	Arg	Pro
	50					55					60				
Trp	Lys	Ser	Ser	Thr	Ile	Ile	Met	Leu	Asn	Leu	Ala	Cys	Thr	Asp	Leu
65					70				75					80	
Leu	Tyr	Leu	Thr	Ser	Leu	Pro	Phe	Leu	Ile	His	Tyr	Tyr	Ala	Ser	Gly
			85						90					95	
Glu	Asn	Trp	Ile	Phe	Gly	Asp	Phe	Met	Cys	Lys	Phe	Ile	Arg	Phe	Ser
		100						105					110		
Phe	His	Phe	Asn	Leu	Tyr	Ser	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Phe	Ser
		115					120					125			
Ile	Phe	Arg	Tyr	Cys	Val	Ile	Ile	His	Pro	Met	Ser	Cys	Phe	Ser	Ile
	130					135					140				
His	Lys	Thr	Arg	Cys	Ala	Val	Val	Ala	Cys	Ala	Val	Val	Trp	Ile	Ile
145					150				155					160	
Ser	Leu	Val	Ala	Val	Ile	Pro	Met	Thr	Phe	Leu	Ile	Thr	Ser	Thr	Asn
			165						170					175	
Arg	Thr	Asn	Arg	Ser	Ala	Cys	Leu	Asp	Leu	Thr	Ser	Ser	Asp	Glu	Leu
		180						185					190		

Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys  
 195 200 205  
 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr  
 210 215 220  
 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg  
 225 230 235 240  
 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro  
 245 250 255  
 Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln  
 260 265 270  
 Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu  
 275 280 285  
 Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val  
 290 295 300  
 Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys  
 305 310 315 320  
 Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn  
 325 330 335

<210> 87  
 <211> 1138  
 <212> DNA  
 <213> H.Sapiens

<400> 87  
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 tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180  
 aaacatgaga aggaactgta acctgattat ggatttgga aaaagataaa tcaacacaca 240  
 aagggaagaaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat 300  
 taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt 360  
 aatgggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc 420  
 acatttcaaa caacttcata ccccaacaaa ttggctcatt cattccatgg ccaactgtgga 480  
 ctttcttctg ggggtgtctgg tcatgcctta cagtatggtg agatctgctg agcactgttg 540  
 gtatttttga gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc 600  
 ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660  
 gagatataaa gccaaagatga atatcttggt tatttggtgtg atgatcttca ttagttggag 720  
 tgtccctgct gtttttgcatt ttggaatgat ctttctggag ctaaaacttca aaggcgctga 780

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 atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt 900  
 ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagtg atgccaatca 960  
 gaagctccaa attggattgg aatgaaaaa tggaaattca caaagcaaag aaaggaaagc 1020  
 tgtgaagaca ttggggattg tgatgggagt tttcctaata tgctgggtgcc ctttctttat 1080  
 ctgtacagtc atggaccctt ttcttcacta cattattcca cctactttga atgatgta 1138

<210> 88  
 <211> 296  
 <212> PRT  
 <213> H.Sapiens

<400> 88

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 Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu  
 20 25 30  
 Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile  
 35 40 45  
 Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser  
 50 55 60  
 Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser  
 65 70 75 80  
 Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys  
 85 90 95  
 Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe  
 100 105 110  
 His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro  
 115 120 125  
 Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile  
 130 135 140  
 Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe  
 145 150 155 160  
 Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val  
 165 170 175  
 His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val  
 180 185 190  
 Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys  
 195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile  
 210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly  
 225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val  
 245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val  
 260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala  
 275 280 285

Arg Gly Ser Arg Ala Asn Ser Ala  
 290 295

<210> 89  
 <211> 1023  
 <212> DNA  
 <213> H.Sapiens

<400> 89  
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 aatgatgtcc gtgcttcct gtacagttta atgggtgetca taattctgac cacactcggt 120  
 ggcaatctga tagttattgt ttctatatca cacttcaaac aacttcatac cccaacaaat 180  
 tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggt catgccttac 240  
 agtatgggtga gatctgctga gcaactgttg tattttggag aagtcttctg taaaattcac 300  
 acaagcaccg acattatgct gagctcagcc tccattttcc atttgtcttt catctccatt 360  
 gaccgctact atgctgtgtg tgatccactg agatataaag ccaagatgaa tatcttggtt 420  
 atttgtgtga tgatcttcat tagttggagt gtccctgctg tttttgcatt tggaatgatc 480  
 tttctggagc taaacttcaa aggcgctgaa gagatatatt acaaacatgt tcaactgcaga 540  
 ggaggttgct ctgtcttctt tagcaaaata tctgggggtac tgacctttat gacttctttt 600  
 tatataacctg gatctattat gttatgtgtc tattacagaa tatatcttat cgctaaagaa 660  
 caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatgaaaaat 720  
 ggaatttcac aaagcaaaga aaggaaagct gtgaagacat tggggattgt gatgggagtt 780  
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 attattccac ctactttgaa tgatgtattg atttggttg gctacttgaa ctctacattt 900  
 aatccaatgg tttatgcatt tttctatcct tgggttagaa aagcactgaa gatgatgctg 960  
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tag

1023

<210> 90  
 <211> 339  
 <212> PRT  
 <213> H.Sapiens

<400> 90

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Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20          25          30
Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35          40          45
Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50          55          60
Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65          70          75          80
Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85          90          95
Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100         105         110
His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115         120         125
Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130         135         140
Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145         150         155         160
Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165         170         175
His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180         185         190
Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195         200         205
Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210         215         220
Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225         230         235         240
Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245         250         255
Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val

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260	265	270
Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val		
275	280	285
Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr		
290	295	300
Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe		
305	310	315
Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu		
325	330	335
Leu Ser Ser		

<210> 91  
 <211> 1696  
 <212> DNA  
 <213> H.Sapiens

<400> 91  
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 ataattactc aaaaggtgat gacaatggcg cagggaggga tgggtgacttg cctggagatg 120  
 cacagcacog tctctcccat actcggtcat tcacaccatc attgattcac caggcaccac 180  
 tccgtgtcca gcaggactct ggggacccca aatggacact accatggaag ctgacctggg 240  
 tgccactggc cacaggcccc gcacagagct tgatgatgag gactcctacc cccaagggtg 300  
 ctgggacacg gtcttctctg tggccctgct gctccttggg ctgccagcca atgggttgat 360  
 ggcgtggctg gccggctccc aggcccgga tggagctggc acgcgtctgg cgctgtcct 420  
 gctcagctg gccctctctg acttcttgtt cctggcagca gcggccttcc agatcctaga 480  
 gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttct 540  
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 cctgctggcg ctgtgccac actggtaccc tgggacccgc ccagtcgcc tgccctctg 660  
 ggtctgcgc ggtgtctggg tgctggccac actcttcagc gtgccctggc tggctctccc 720  
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 gctgtcgtg aggatgctg aggtcctggg gggttctctg cctttcctcc tgctgctcgt 840  
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 agcctgcgg ggcttcgcc gtgtggccag gaccattctg tcagcctatg tggctctgag 960  
 gctgccctac cagctggccc agctgctcta cctggccttc ctgtgggacg tctactctg 1020  
 ctacctgctc tgggaggccc tggctactc cgactacctg atcctactca acagctgcct 1080



cagcccccttc ctctgcctca tggccagtgc cgacctccgg acctgtgtgc gctccgtgct 1140  
 ctogtccttc gcggcagctc tctgcgagga gcggccgggc agcttcacgc ccaactgagcc 1200  
 acagacccag ctagattctg aggggtccaac tctgccagag ccgatggcag aggccagtc 1260  
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 cacagctcag ccacagctga accctacggc ccagccacag tcggatccca cagcccagcc 1380  
 acagctgaac ctcatggccc agccacagtc agattctgtg gccagccac aggcagacac 1440  
 taacgtccag acccctgcac ctgctgccag ttctgtgccc agtccctgtg atgaagcttc 1500  
 cccaaccca tctcgcctc ctaccccagg ggcccttgag gaccagcca cacctcctgc 1560  
 ctctgaagga gaaagcccca gcagcaccac gccagaggcg gcccggggcg caggcccccac 1620  
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 gaaccagcca gtcaga 1696

<210> 92  
 <211> 505  
 <212> PRT  
 <213> H.Sapiens

<400> 92

Leu Ala Trp Arg Cys Thr Ala Pro Ser Leu Pro Tyr Ser Val Ile His  
 1 5 10 15  
 Thr Ile Ile Asp Ser Pro Gly Thr Thr Pro Cys Pro Ala Gly Leu Trp  
 20 25 30  
 Gly Pro Gln Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly  
 35 40 45  
 His Arg Pro Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly  
 50 55 60  
 Gly Trp Asp Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro  
 65 70 75 80  
 Ala Asn Gly Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly  
 85 90 95  
 Ala Gly Thr Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp  
 100 105 110  
 Phe Leu Phe Leu Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His  
 115 120 125  
 Gly Gly His Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe  
 130 135 140  
 Leu Trp Gly Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu  
 145 150 155 160

Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly  
 165 170 175  
 His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val  
 180 185 190  
 Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala  
 195 200 205  
 Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu  
 210 215 220  
 Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe  
 225 230 235 240  
 Leu Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg  
 245 250 255  
 Thr Cys His Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg  
 260 265 270  
 Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr  
 275 280 285  
 Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser  
 290 295 300  
 Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu  
 305 310 315 320  
 Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp  
 325 330 335  
 Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu  
 340 345 350  
 Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln  
 355 360 365  
 Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln  
 370 375 380  
 Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln  
 385 390 395 400  
 Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln  
 405 410 415  
 Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln  
 420 425 430  
 Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln  
 435 440 445  
 Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala  
 450 455 460  
 Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro

465                                      470                                      475                                      480  
 Ala Thr Pro Pro Ala Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro  
    485                                      490                                      495

Glu Ala Ala Pro Gly Ala Gly Pro Thr  
    500                                      505

<210> 93  
 <211> 1413  
 <212> DNA  
 <213> H.Sapiens

<400> 93  
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 gatgatgagg actcctaccc ccaaggtggc tgggacacgg tcttcctggt ggccctgctg 120  
 ctccttgggc tgccagccaa tgggttgatg gcgtggctgg ccggctccca ggcccgcat 180  
 ggagctggca cgcgtctggc gctgctctctg ctccagctgg cctctctctga cttcttgttc 240  
 ctggcagcag cggccttcca gatectagag atccggcatg ggggacactg gccgctgggg 300  
 acagctgcct gccgcttcta ctacttcta tggggcgtgt cctactcctc cggcctcttc 360  
 ctgctggccg ccctcagcct cgaccgctgc ctgctggcgc tgtgccaca ctggtaccct 420  
 gggcaccgcc cagtccgcct gcccctctgg gtctgcgccg gtgtctgggt gctggccaca 480  
 ctcttcagcg tgccctggct ggtcttcccc gaggtgccg tctggtggtg cgacctggtc 540  
 atctgcctgg acttctggga cagcgaggag ctgtcgctga ggatgctgga ggtcctgggg 600  
 ggcttctctgc ctttctcct gctgctctgc tgccacgtgc tcaccaggc cacagcctgt 660  
 cgcacctgcc accgccaaca gcagcccgca gcctgccggg gcttcgcccg tgtggccagg 720  
 accattctgt cagcctatgt ggtcctgagg ctgccctacc agctggcca gctgctctac 780  
 ctggccttcc tgtgggacgt ctactctggc tacctgctct gggaggccct ggtctactcc 840  
 gactacctga tcctactcaa cagctgcctc agccccttcc tctgctcat ggccagtgcc 900  
 gacctccgga cctgctgctg ctccgtgctc tcgtccttcg cggcagctct ctgcgaggag 960  
 cggccgggca gcttcacgcc cactgagcca cagaccagc tagattctga ggtccaact 1020  
 ctgccagagc cgatggcaga ggcccagtca cagatggatc ctgtggcca gcctcaggtg 1080  
 aacccacac tccagccacg atcggatccc acagctcagc cacagctgaa ccctacggcc 1140  
 cagccacagt cggatccac agcccagcca cagctgaacc tcatggcca gccacagtca 1200  
 gactctgtgg ccagccaca ggcagacact aacgtccaga cccctgcacc tgctgccagt 1260  
 tctgtgcca gtccctgtga tgaagcttcc ccaaccccat cctcgcatcc taccaggg 1320  
 gcccttgagg acccagccac acctcctgcc tctgaaggag aaagcccag cagacccccg 1380

ccagaggcgg ccccgggcgc aggcccccacg tga

1413

<210> 94  
 <211> 419  
 <212> PRT  
 <213> H.Sapiens

<400> 94

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Arg	Thr	Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly	Gly	Trp	Asp	20	25	30	
Thr	Val	Phe	Leu	Val	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Pro	Ala	Asn	Gly	35	40	45	
Leu	Met	Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly	Ala	Gly	Thr	50	55	60	
Arg	Leu	Ala	Leu	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	Phe	Leu	Phe	65	70	75	80
Leu	Ala	Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	Gly	Gly	His	85	90	95	
Trp	Pro	Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe	Leu	Trp	Gly	100	105	110	
Val	Ser	Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu	Ser	Leu	Asp	115	120	125	
Arg	Cys	Leu	Leu	Ala	Leu	Cys	Pro	His	Trp	Tyr	Pro	Gly	His	Arg	Pro	130	135	140	
Val	Arg	Leu	Pro	Leu	Trp	Val	Cys	Ala	Gly	Val	Trp	Val	Leu	Ala	Thr	145	150	155	160
Leu	Phe	Ser	Val	Pro	Trp	Leu	Val	Phe	Pro	Glu	Ala	Ala	Val	Trp	Trp	165	170	175	
Tyr	Asp	Leu	Val	Ile	Cys	Leu	Asp	Phe	Trp	Asp	Ser	Glu	Glu	Leu	Ser	180	185	190	
Leu	Arg	Met	Leu	Glu	Val	Leu	Gly	Gly	Phe	Leu	Pro	Phe	Leu	Leu	Leu	195	200	205	
Leu	Val	Cys	His	Val	Leu	Thr	Gln	Ala	Thr	Ala	Cys	Arg	Thr	Cys	His	210	215	220	
Arg	Gln	Gln	Gln	Pro	Ala	Ala	Cys	Arg	Gly	Phe	Ala	Arg	Val	Ala	Arg	225	230	235	240
Thr	Ile	Leu	Ser	Ala	Tyr	Val	Val	Leu	Arg	Leu	Pro	Tyr	Gln	Leu	Ala	245	250	255	

Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu  
                   260                  265                  270  
 Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser  
                   275                  280                  285  
 Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr  
                   290                  295                  300  
 Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu  
                   305                  310                  315                  320  
 Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser  
                   325                  330                  335  
 Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met  
                   340                  345                  350  
 Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser  
                   355                  360                  365  
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser  
                   370                  375                  380  
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser  
                   385                  390                  395                  400  
 Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala  
                   405                  410                  415  
 Pro Ala Ala

<210> 95  
 <211> 49  
 <212> DNA  
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<220>  
 <221> misc\_feature  
 <223> Novel Sequence

<400> 95  
 ttcaaagctt atggaatcat ctttctcatt tggagtgatc cttgctgtc

49

<210> 96  
 <211> 49  
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<220>  
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<400> 96  
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49

<210> 97  
<211> 22  
<212> DNA  
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<223> Novel Sequence

<400> 97  
gctcaaccca ctcatttatg cc 22

<210> 98  
<211> 22  
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<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 98  
aaactttctt gcccttaccg tc 22

<210> 99  
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<221> misc\_feature  
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<400> 99  
aaagcagcac cccgaatacc 20

<210> 100  
<211> 21  
<212> DNA  
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<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 100  
catgatcaac ctgagcgtca c 21

<210> 101

<211> 28  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 101  
ttcaaagctt atggagtcgg ggctgctg

28

<210> 102  
<211> 30  
<212> DNA  
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<223> Novel Sequence

<400> 102  
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<400> 103  
gcacacctggc cgctatctgt gcactctacg

30

<210> 104  
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<223> Novel Sequence

<400> 104  
cgtagagtgc acagatagcg gccaggatgc

30

<210> 105  
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<400> 105  
aaccatcatca tctacacgc 19

<210> 106  
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<212> DNA  
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<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 106  
tgcctgtgga gccgctgg 18

<210> 107  
<211> 33  
<212> DNA  
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<223> Novel Sequence

<400> 107  
gcataagctt ccatgtacaa cgggtcgtgc tgc 33

<210> 108  
<211> 33  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 108  
gcattctaga tcagtgccac tcaacaatgt ggg 33

<210> 109  
<211> 20  
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<223> Novel Sequence

<400> 109  
gaagcccagc actgtttacc 20

<210> 110  
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<212> DNA  
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<400> 110  
tgaaatacct gtccgcagcc 20

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<223> Novel Sequence

<400> 111  
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<210> 112  
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<400> 112  
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<210> 113  
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<400> 113  
cagcccaaac atccaagtc 19

<210> 114  
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<400> 114  
acccactta atcagcctc 19

<210> 115  
<211> 34  
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<400> 115  
gatcgaattc gcaggagcaa tgaaaatcag gaac 34

<210> 116  
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<212> DNA  
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<400> 116  
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<210> 117  
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<400> 117  
acagcccaa agccaaacac 20

<210> 118  
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<212> DNA  
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<400> 118  
ccgcaggagc aatgaaaatc ag 22

<210> 119  
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<400> 119  
ctgaaagttg tcgctgacc 19

<210> 120  
<211> 21  
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<400> 120  
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<210> 121  
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<400> 121  
gcataccatg aatgagccac tagac 25

<210> 122  
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<212> DNA  
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<220>  
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<400> 122  
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<210> 123  
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<400> 123  
ctgtctctct gtcctcttcc 20

<210> 124  
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<400> 124  
gcaccgatct tcattgaatt tc 22

<210> 125  
<211> 22  
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<400> 125  
acttcaaaca acttcatacc cc 22

<210> 126  
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<400> 126  
acacacagca tagtagcg 18

<210> 127  
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<400> 127

cagagcttga tgatgaggac

20

<210> 128  
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<400> 128  
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<210> 129  
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<220>  
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<400> 129

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<210> 130  
<211> 52  
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<220>  
<221> misc\_feature  
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<400> 130  
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52

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<220>  
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<223> Novel Sequence

<400> 131  
tgccacactg atgcaactcc

20

<210> 132  
<211> 48  
<212> DNA  
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<400> 132  
gcgtatatac actcactata gggagacctg ccacactgat gcaactcc 48

<210> 133  
<211> 24  
<212> DNA  
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<400> 133  
gcgtgtctgc tagactctat ttcc 24

<210> 134  
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<400> 134  
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<210> 137  
<211> 23  
<212> DNA  
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<223> Novel Sequence

<400> 137  
gctacgccac tctttactat ccc

23

<210> 138  
<211> 49  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 138  
gcgtaatagc actcactata gggagacctt atgagcagca attcatccc

49

<210> 139  
<211> 20  
<212> DNA  
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<220>  
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<400> 139  
cacacccacc aagaaatcag

20

<210> 140  
<211> 48  
<212> DNA  
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<400> 140  
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48

<210> 141

<211> 21  
<212> DNA  
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<400> 141  
ttatgagcag caattcatcc c

21

<210> 142  
<211> 49  
<212> DNA  
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<220>  
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49

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<212> DNA  
<213> Artificial Sequence

<220>  
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<223> Novel Sequence

<400> 143  
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19

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<220>  
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50

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<212> DNA  
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<400> 145  
cgattatcca cactttgacc c

21

<210> 146  
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50

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<400> 147  
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19

<210> 148  
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<400> 148  
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48

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<212> DNA  
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<400> 149  
ctgtaaaatt cacacaagca cc 22

<210> 150  
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<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 150  
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<210> 151  
<211> 31  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 151  
gcatgaattc acaatgccag tgataaggaa g 31

<210> 152  
<211> 31  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 152  
gatcaagctt ggaatgatgc ccttttgcca c 31

<210> 153  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> .153  
gatcctcgag catcattcaa agtaggtgg 29

<210> 154  
<211> 42  
<212> DNA  
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<223> Novel Sequence

<400> 154  
gatcctcgag ctatgaactc aattccaaaa ataatttaca cc 42

<210> 155  
<211> 49  
<212> DNA  
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<220>  
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<400> 155  
gctacttgaa ctctacattt aatccaatgg tttatgcatt tttctatcc 49

<210> 156  
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<212> DNA  
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<400> 157  
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<400> 158  
gatcctcgag tcacgtgggg cctgcgcccg g 31

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<400> 159  
gcgtaatacg actcactata gggagaccgc gtgtctgcta gactctatTT cc 52

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<400> 160  
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<210> 161  
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<400> 161  
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<210> 162  
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<400> 162  
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24

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<400> 163  
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50

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<400> 164  
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24

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52

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23

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49

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48

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<210> 171  
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<400> 171  
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<400> 172  
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<210> 173  
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<400> 174

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<400> 176  
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19

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<400> 177  
gcgtaatacg actcactata gggagaccag aagacagagc aacctcc

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<400> 178  
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22



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<400> 179  
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31

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<400> 180  
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<400> 181  
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<400> 182  
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22

<210> 183  
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<400> 183

ctgtctctct gtcctcttcc

20

<210> 184

<211> 22

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<400> 184

gcaccgatct tcattgaatt tc

22

<210> 185

<211> 1188

<212> DNA

<213> H.Sapiens

<400> 185

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ctatccaacg	cactgggtgct	gctttgttgc	gcctacagcg	ctgagctccg	cactcgagcc	180
tcaggcgctc	tctggtgaa	tctgtctctg	ggccacctgc	tgctggcggc	gctggacatg	240
cccttcacgc	tgctcggtgt	gatgcgcggg	cggacaccgt	cggcgccccg	cgcatgccaa	300
gtcattggct	tcctggacac	cttcctggcg	tccaacgcgg	cgctgagcgt	ggcggcgctg	360
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ttcgtgctgc	cgctggcggt	gctctgcctc	acctcgctcc	aggtgcaccg	ggtggcacgc	660
agacactgcc	agcgcgatga	caccgtcacc	atgaaggcgc	tcgcgctgct	cgccgacctg	720
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aggctggcgg agctcgtgcc ctctcgtcacc gtgaacgccc agtggggcat cctcagcaag 900  
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 ttccgccaag tcctggccgg catggtgcac cggctgctga agagaacccc gcgcccagca 1020  
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 ccgcgcccag cgtccaccca caacggctct gtggacacag agaattgattc ctgcctgcag 1140  
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<210> 186  
 <211> 363  
 <212> PRT  
 <213> H.Sapiens

<400> 186

Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu  
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 Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr  
 20 25 30  
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu  
 35 40 45  
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu  
 50 55 60  
 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln  
 65 70 75 80  
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser  
 85 90 95  
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu  
 100 105 110  
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly  
 115 120 125  
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys  
 130 135 140  
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu  
 145 150 155 160  
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu  
 165 170 175  
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser  
 180 185 190  
 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr  
 195 200 205

Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val  
 210 215 220

Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr  
 225 230 235 240

Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro  
 245 250 255

Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn  
 260 265 270

Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val  
 275 280 285

Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val  
 290 295 300

Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala  
 305 310 315 320

Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu  
 325 330 335

Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp  
 340 345 350

Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His  
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<400> 187  
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29

<210> 188  
 <211> 28  
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<220>  
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<400> 188  
 gcattctaga cctcagtgtg tctgctgc

28

<210> 189

<211> 20  
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<220>  
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<223> Novel Sequence

<400> 189  
tgctgctttg ttgcgcctac

20

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<400> 190  
ttggacgcca ggaaggtg

18